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(54) Title: CHIMERIC PROTEINS INCLUDING PROTEASE NEXIN-1 VARIANTS			
(57) Abstract			
Chimeric proteins, also referred to herein as variants, and methods of producing, formulating and utilizing such proteins are disclosed. Five different general types of variants are disclosed.			
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CHIMERIC PROTEINS INCLUDING PROTEASE NEXIN-1 VARIANTSField of the Invention

5 This invention relates generally to the field of proteins, protein analogs, and methods of specifically altering proteins in order to change their biological activity. More particularly, the invention relates to identifying the active site of a protein, for example, 10 Protease Nexin-1, and altering the active site by changing one or more amino acids therein to create an analog or replacing the active site of a protein with the active site of a completely different protein to create a chimeric protein. The invention also relates to 15 identifying cysteine residues, or amino acid residues which may be substituted by cystine without abolishing activity, and attaching polyethylene glycol to the thio group of cysteine, thereby increasing protein stability.

Background of the Invention

20 It has been known for some time that proteins have specific functions in the body. For example, natural physiological functions such as tissue remodeling, inflammation, coagulation, and fibrinolysis require proteolytic enzymes. Of particular importance is a 25 mechanistic class of proteases called serine proteases. It is also known that the active site of all functional members of the serine protease family contains a characteristic catalytic triad consisting of serine (hence the name), aspartic acid and histidine. The 30 hydroxyl group of the catalytic site serine is involved in a nucleophilic attack on the carbonyl carbon of the peptide bond to be hydrolyzed resulting in acylation of the protease and hydrolysis of the peptide bond. This is

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followed rapidly by a deacylation step resulting in the release of intact protease.

In order to provide examples of the present invention the inventors have focused on Protease nexin-1 (PN-1) which is a serine protein purified from serum-free medium conditioned by human foreskin cells (Scott, R.W. et al., J Biol Chem (1983) 58:1043910444). It is a 42 kd glycoprotein which is released by fibroblasts, myotubes, heart muscle cells, and vascular smooth muscle cells. Its release, along with that of plasminogen activator, is stimulated by phorbol esters and by mitogens (Eaton, D.L. et al., J Cell Biol (1983) 123:128). Native PN-1 is an approximately 400 amino acid protein containing about 10% carbohydrate. Since it is present only in trace levels in serum, it apparently functions at or near the surfaces of interstitial cells. PN-1 inhibits all the known activators of urokinase proenzyme, plasmin, trypsin, thrombin, and Factor Xa (Eaton, D.L. et al., J Biol Chem (1984) 259:6241). It also inhibits tissue plasminogen activator and urokinase. However, PN-1 does not inhibit elastase or cathepsin G.

In our earlier application now U. S. Patent 5,187,089 we noted that the reactive site region of PN-1 acts as a substrate analogue and postulated that it might be possible to drastically alter PN-1 activity by modifying the reactive site sequence of PN-1, thus changing its protease specificity. Similar efforts with α -1-antitrypsin, for example, resulted in variants with altered and therapeutic potential (M. Courtney et al., Nature (1985) 313:149-151). PN-1 is different from most serpins in that it is found in tissues, contains a high affinity heparin binding site which localizes it to tissues, and has a tissue clearance receptor that is responsible for endocytosis of protease-PN-1 complexes. We were able to generate PN-1 variants as inhibitors of

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physiologic proteases such as elastase and thereby provide useful pharmaceutically active compounds.

We have now invented a number of additional PN-1 variants, including variants which inactivate elastase and cathepsin G, and have moved well beyond our prior work to provide variants and methods for designing and producing such variants which have significantly altered protease specificity and second-order association rate constants with respect to a variety of serine proteases. In addition, we provide variants and methods of producing such variants which have polyethylene glycol specifically attached to one or more cysteine residues, such cysteine residues being either present in the parent molecule or introduced on the surface of the protein by site-directed mutagenesis, and methods for determining appropriate sites for the introduction of cysteine residues. In addition, we provide variants and methods of producing such variants which combine the specific localization ability of a receptor-binding protein with the protease-inhibiting activity of PN-1 or variant thereof, resulting in desired biological activities with particular substrates.

Summary of the Invention

Chimeric proteins, also referred to herein as variants, and methods of producing, formulating and utilizing such proteins are disclosed. Five different general types of variants are disclosed. A Type I variant of the invention is produced by site-directed mutagenesis wherein a single amino acid within the active site of PN-1 is substituted with an amino acid different from the naturally-occurring amino acid at that position. A Type II variant of the invention is similar to a Type I variant in that the active site of PN-1 is changed. However, to produce a Type II variant, the active site of

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PN-1 is changed so as to match the active site of another serpin which change many require one or more amino acid substitutions, deletions or additions. A Type III variant of the invention is produced whereby the active site or a portion thereof of PN-1 is substituted with a sequence which corresponds to the substrate sequence for a particular protease. A Type IV variant is produced wherein a cysteine residue, which is either present in the native protein or introduced by site-specific mutation, is used to attach polyethylene glycol. A Type V variant of the invention involves producing a fusion protein wherein PN-1 is fused to the receptor binding region of another protein in order to localize PN-1 to a different receptor. Variants of Type I, II or III are referred to herein as variants. The compounds of Type IV wherein polyethylene glycol is attached to a thio group are referred to as cysteine-PEGylation proteins, and the compounds of Type V are referred to as fusion proteins or chimeric proteins.

Embodiments of the present invention provide pharmaceutical compositions which contain one or more variants of all or any of Type I, II, III, IV or V.

An important object of the invention is to provide a wide range of different variants, and in particular PN-1-variants, having a particular and desired biological activity.

Another object is to provide PN-1 variants using site-directed mutagenesis in order to change a single amino acid within the active site of PN-1.

Another important object is to provide a PN-1-variant wherein the active site of PN-1 is specifically modified so as to match the active site of another enzyme inhibitor, preferably another serpin.

Yet another important object of the present invention is to provide variants such as protease nexin-1

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variants which include, in PN-1, the substrate sequence for a different protease, making it possible to inhibit the activity of that protease.

Still another important object is to provide
5 proteins which are PEGylated by attachment to a thio group, i.e. the polyethylene glycol is attached to a cysteine amino acid within a protein, which cysteine amino acid of the protein is not involved in a disulfide bond.

10 Another important object is to provide a method of attaching polyethylene glycol to a protein by first subjecting the protein to site-directed mutagenesis to add a cysteine residue at a position where the protein or a structurally related protein is normally glycosylated,
15 and thereafter attaching the polyethylene glycol to the cysteine residue.

Another important object is to provide a method of attaching PEG to a protein by first subjecting the protein to site-directed mutagenesis to add a cysteine
20 residue at a position on the surface of the protein, and thereafter attaching the PEG to the cysteine residue.

Another important object is to provide dimeric or multimeric proteins cross-linked by reaction with a reagent composed of PEG having two protein-reactive
25 moieties.

Yet another important object is to provide fusion proteins wherein the receptor binding region of another protein is connected to PN-1 in order to localize PN-1 to a different receptor.

30 Another object of the present invention is to provide a pharmaceutical composition comprising excipient carrier materials having a compound of the invention dispersed therein.

Another object of the present invention is to
35 provide therapeutic methods of treatment which involve

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administering to a patient in need thereof a pharmaceutically effective amount of a composition comprising excipients and a compound of the invention.

A feature of the present invention is that the
5 variants can be designed to have a specific receptor-binding domain while maintaining the natural biological activity of the protein to which the new binding domain is attached.

An advantage of the present invention is that the
10 variants have substantially different inhibitory effects on certain proteolytic enzymes as compared to the natural protein.

Another object of the present invention is to provide variants useful in treating diseases associated
15 with a specific biological activity.

Yet another advantage of the present invention is to describe and disclose variants which are useful in treating elastase-related diseases.

Another feature of the present invention is that
20 certain variants have substantially altered protease specificity as compared with the natural protein.

Another advantage of the present invention is that certain variants have substantially greater second order association rate constants with respect to particular
25 serine proteases as compared with the second order association rate constant of natural proteins with respect to such serine proteases.

Another advantage of the present invention is that certain variants have substantially slower second order
30 association rate constants with respect to particular serine proteases as compared with the second order association rate constant of natural proteins with respect to such serine proteases.

Yet another object is to provide methods of
35 delivery such as by injection, intranasal and

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interpulmonary delivery which methods are carried out using pharmaceutical compositions in the form of injectable formulations, spray formulations and aerosols.

Another advantage is that biologically stabilized proteins can be produced by attaching the polyethylene glycol to a cysteine residue of the protein.

Another advantage is to provide methodology for readily attaching polyethylene glycol molecules to proteins at a cysteine residue of the protein which are preferably located at native sites of glycosylation.

Yet another advantage is that amino acid residues for substitution with cysteine may be selected so that subsequent attachment of polyethylene glycol to the thio group of the substituted cysteine residue increases biological stability of the cysteine-PEGylated protein relative to wild type without abolishing biological activity.

Another advantage is that proteins which normally require glycosylation for biological stability may be produced commercially by expression in a prokaryotic host or other host which does not provide for glycosylated recombinant proteins. After expression of the protein by the prokaryotic host, biological stability of the protein can be increased by attachment of polyethylene glycol to a native or engineered cysteine residue in the protein.

Another advantage is that cysteine-PEGylated proteins can be produced without exposing the protein to highly toxic chemicals such as dioxane, cyanuric chloride, DMF, or other chemicals used in conventional methods for attaching polyethylene glycol to a protein.

These and other objects, advantages and features of the present invention will become apparent to those persons skilled in the art upon reading the details of the structure, synthesis, formulation and usage as more

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fully set forth below reference being made to the accompany figures forming a part hereof.

Brief Description of the Drawings

Figure 1 shows the nucleotide sequence of the coding region and the deduced amino acid sequence of PN-1 α ; and

Figure 2 shows the nucleotide sequence of the coding region and the deduced amino acid sequence of PN-1 β .

Figure 3 is a schematic drawing of a three-dimensional structure of PN-1 as determined by X-ray crystallography. The approximate position of residues of particular interest are shown according to their relative position within a given helix (h) or β -sheet (s). The helices and β -sheets of the PN-1 protein are each assigned letters (e.g. A, B, etc.) (Engh, et al. 1990 *Protein Engin.* 3(6):469-477).

Figure 4 is a graph which shows the activity of samples of reaction mixtures containing cysteine-PEGylated PN-1 variants (N99C;N140C) produced by the method of the invention (open squares) and the activity of samples of reaction mixtures containing a PEGylated PN-1 variant (N99C;N140C) produced by a conventional method (closed diamonds).

Detailed Description of the Preferred Embodiment

Before the present compounds, variants, formulations and methods for making and using such are described, it is to be understood that this invention is not limited to the particular compounds, variants, formulations or methods described, as such variants, formulations and methodologies may, of course, vary. It is to be understood that the terminology used herein is for the purpose of describing particular embodiments

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only, and is not intended to be limiting since the scope of the present invention will be limited only by the appended claims.

It must be noted that as used in the specification and the appended claims, the singular forms "a", "an" and "the" include plural referents unless the context clearly dictates otherwise. Thus, for example, reference to "a protease nexin-1 variant" includes mixtures of such variants, reference to "an analog" includes reference to mixtures of such analogs and reference to "the method of treatment" includes reference to one or more methods of treatment of the type which will be known to those skilled in the art or will become known to them upon reading this specification, and so forth.

15 A. Definitions

As used herein, "protease nexin-1" and "PN-1" are used interchangeably and refer to DNA codons and resulting amino acid sequences which make up PN-1 α and PN-1 β which are shown respectively in Figures 1 and 2. PN-1 is distinguishable from the two other protease nexin factors, PN-II and PN-III (Knauer, D.J. et al., J Biol Chem (1982) 257:15098-15104), which are also thrombin inhibitors, but are less strongly binding to this protease and are of different molecular weight, three-dimensional structure and mechanism of function.

The terms "variants", "protein variants" and "chimeric proteins" are used interchangeably herein to refer to any amino acid sequence which corresponds to the amino acid sequence of a natural protein or a biologically active portion of a natural protein except that some change has been made in the structures. Typical changes per the present invention involve:

(1) one or more amino acids within the natural sequence is replaced with one or more amino acids different from

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the amino acids present in the natural protein; and/or
(2) one or more amino acids has been added to the natural
sequence, and the addition of such amino acids changes
the biological activity of the variant; and/or (3) one or
5 more amino acids is deleted from the natural sequence;
and/or (4) polyethylene glycol is bound to a thio group
of a natural or artificially introduced cysteine residue
of a sequence; and/or (5) two naturally occurring
sequences are fused together, i.e. two sequences not
10 normally connected are fused.

"Protease nexin-1 variants" and "analogs of
protease nexin-1" are terms which are used synonymously
herein to define a Type I variant and are thereby
encompassed by the term "variant." The terms are
15 intended to refer generally to proteins wherein one or
more of the amino acids within protease nexin-1 have been
substituted with a different amino acid. More
specifically, the protease nexin-1 variants of the
invention include substantially the same amino acid
20 sequence as protease nexin-1 but for the substitution of
different amino acids at or near the active site.
Specifically, substitutions of different amino acids can
be made at any of P_1 , P_2 , P_3 , P_4 sites and/or made at the
 P_1' , P_2' , or P_3' , P_4' sites. Although other substitutions
25 and deletions of amino acids in the sequence of protease
nexin-1 are encompassed by this invention, the
substitutions at or near the active site are most
important with respect to changing the specificity and/or
reactivity of the variant with respect to particular
30 proteases. Particularly preferred protease nexin-1
variants of the invention are variants which have high
activity relative to a substrate to which natural PN-1
has little or no activity such as variants which inhibit
elastase and, more particularly, which inhibit elastase
35 and have their ability to inhibit elastase enhanced in

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the presence of heparin and/or heparin-like compounds. Other preferred protease nexin-1 variants, for example, have increased ability to inhibit urokinase and/or another serine protease as compared with protease

5 nexin-1.

"Control sequence" refers to a DNA sequence or sequences which are capable, when properly ligated to a desired coding sequence, of effecting its expression in hosts compatible with such sequences. Such control
10 sequences include at least promoters in both procaryotic and eucaryotic hosts, and preferably, transcription termination signals. Additional factors necessary or helpful in effecting expression may also be identified. As used herein, "control sequences" simply refers to
15 whatever DNA sequence may be required to effect expression in the particular host used.

"Cells" or "cell cultures" or "recombinant host cells" or "host cells" are often used interchangeably as will be clear from the context. These terms include the
20 immediate subject cell, and, of course, the progeny thereof. It is understood that not all progeny are exactly identical to the parental cell, due to chance mutations or differences in environment. However, such altered progeny are included in these terms, so long as
25 the progeny retain the characteristics relevant to those conferred on the originally transformed cell. In the present case, for example, such a characteristic might be the ability to produce recombinant PN-1.

"purified" or "pure" refers to material which is
30 free from substances which normally accompany it as found in its native state. Thus "pure" PN-1-encoding DNA refers to DNA which is found in isolation from its native environment and free of association with DNAs encoding other proteins normally produced by cells natively
35 producing PN-1. "Pure" PN-1 refers to PN-1 which does

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not contain materials normally associated with its in situ environment in human or other mammalian tissue. Of course, "pure" PN-1 may include materials in covalent association with it, such as glycoside residues or materials introduced for, for example, formulation as a therapeutic. The term "pure" also includes variants wherein compounds such as polyethylene glycol, Biotin or other moieties are bound to the variant in order to allow for the attachment of other compounds and/or provide for formulations useful in therapeutic treatment or diagnostic procedures. "Pure" simply designates a situation wherein the substance referred to is, or has been, isolated from its native environment and materials which normally accompany it. Of course, the DNA claimed herein as purified and free of substances normally accompanying it, but encoding PN-1, can include additional sequence at the 5' and/or 3' end of the coding sequence which might result, for example, from reverse transcription of the noncoding portions of the message when the DNA is derived from a cDNA library or might include the reverse transcript for the signal sequence as well as the mature protein encoding sequence.

"Degenerate with", as referred to a DNA sequence, refers to nucleotide sequences encoding the same amino acid sequence as that referenced.

"Operably linked" refers to a juxtaposition wherein the components are configured so as to perform a desired function such as their natural biochemical function. Thus, control sequences or promoters operably linked to a coding sequence are capable of effecting the expression of the coding sequence.

"Heparin", "heparan sulfate" and "heparin-like compounds" are terms which are used synonymously herein. Each of the terms singly or in combination with the others is intended to encompass a large group of

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compounds which are generally described as sulfated polysaccharides, which includes proteoglycans and glycosaminoglycans (GAG) which are alternating copolymers of a hexosamine and an aldouronic acid. These copolymers are found in sulfated forms and are synthesized as proteoglycans and are collectively referred to as mucopolysaccharides. Other compounds such as dextran sulfate are considered "heparin-like" for purposes of the invention. Similar alternating copolymers, especially those which are highly sulfated and thus very negatively charged, are useful "heparin-like" compounds in this invention. Extensive information with respect to "heparin", "heparin-like compounds" such as glycosaminoglycans are described in detail by Benito Casu, "Structure and Biological Activity of Heparin", published in Advances in Carbohydrate Chemistry and Biochemistry, Vol. 43, pp. 51-134, which is incorporated herein by reference to disclose such compounds which might be useful in combination with certain PN-1 variants disclosed herein.

A description of the invention is facilitated by listing the relationship between the one-letter symbols and the three-letter abbreviations for amino acids as follows:

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<u>One-Letter Symbols</u>		<u>Three-Letter</u>
<u>Abbreviations</u>		
A	alanine	ala
C	cysteine	cys
5 D	aspartic acid	asp
E	glutamic acid	gln
F	phenylalanine	phe
G	glycine	gly
H	histidine	his
10 I	isoleucine	ile
K	lysine	lys
L	leucine	leu
M	methionine	met
N	asparagine	asn
15 P	proline	pro
Q	glutamine	gln
R	arginine	arg
S	serine	ser
T	threonine	thr
20 V	valine	val
W	tryptophan	trp
Y	tyrosine	tyr

Amino acids have the following general structural formula



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and are classified based on the chemical composition of the "R" group as follows:

1. Aliphatic
2. Hydroxyl
- 5 3. Sulfur
4. Aromatic
5. Acidic (and amides)
6. Basic
7. Imino

10 Naturally occurring amino acids can be generally classified as being polar or non-polar as follows:

Polar S, T, C, Y, D, N, E, Q, R, H, K

Non-polar G, A, V, L, I, M, F, W, P

15 It is the "R" group which determines whether the amino acid will be polar or non-polar.

Amino acid residues can be generally subclassified into four major subclasses as follows:

20 Acidic: The residue has a negative charge due to loss of H ion at physiological pH and the residue is attracted by aqueous solution so as to seek the surface positions in the conformation of a peptide in which it is contained when the peptide is in aqueous medium at physiological pH.

25 Basic: The residue has a positive charge due to association with H ion at physiological pH and the residue is attracted by aqueous solution so as to seek the surface positions in the conformation of a peptide in which it is contained when the peptide is in aqueous medium at physiological pH.

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Neutral/non-polar: The residues are not charged at physiological pH and the residue is repelled by aqueous solution so as to seek the inner positions in the conformation of a peptide in which it is contained when
5 the peptide is in aqueous medium. These residues are also designated "hydrophobic" herein.

Neutral/polar: The residues are not charged at physiological pH, but the residue is attracted by aqueous solution so as to seek the outer positions in the
10 conformation of a peptide in which it is contained when the peptide is in aqueous medium.

It is understood, of course, that in a statistical collection of individual residue molecules some molecules will be charged, and some not, and there will be an
15 attraction for or repulsion from an aqueous medium to a greater or lesser extent. To fit the definition of "charged", a significant percentage (at least approximately 25%) of the individual molecules are charged at physiological pH. The degree of attraction or
20 repulsion required for classification as polar or non-polar is arbitrary, and, therefore, amino acids specifically contemplated by the invention have been specifically classified as one or the other. Most amino acids not specifically named can be classified on the
25 basis of known behavior.

Amino acid residues can be further subclassified as cyclic or noncyclic, and aromatic or nonaromatic, self-explanatory classifications with respect to the side chain substituent groups of the residues, and as small or
30 large. The residue is considered small if it contains a total of 4 carbon atoms or less, inclusive of the carboxyl carbon. Small residues are, of course, always nonaromatic.

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For the naturally occurring protein amino acids, subclassification according to the foregoing scheme is as follows:

Acidic: Aspartic acid and Glutamic acid;

5 Basic/noncyclic: Arginine, Lysine;

Basic/cyclic: Histidine;

Neutral/polar/small: Threonine, Serine and Cysteine;

10 Neutral/polar/large/nonaromatic: Threonine, Asparagine, Glutamine;

Neutral/polar/large/aromatic: Tyrosine;

Neutral/non-polar/small: Alanine;

Neutral/non-polar/large/nonaromatic: Valine, Isoleucine, Leucine, Methionine;

15 Neutral/non-polar/large/aromatic: Phenylalanine and Tryptophan.

Proline

The gene-encoded amino acid proline, although technically within the group neutral/non-polar/large/ cyclic and nonaromatic, is a special case due to its known effects on the secondary conformation of peptide chains, and is not, therefore, included in this defined group, but is included as a group of its own.

20 Other amino acid substitutions for those encoded in the gene can also be included in peptide compounds

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within the scope of the invention and can be classified within this general scheme.

Variants of the invention may include commonly encountered amino acids, which are not encoded by the genetic code, for example, β -alanine (β -ala), or other omega-amino acids, such as 3-amino propionic, 4-amino butyric and so forth, α -aminoisobutyric acid (Aib), sarcosine (Sar), ornithine (Orn), citrulline (Cit), t-butylalanine (t-BuA), t-butylglycine (t-BuG), N-methylisoleucine (N-MeIle), phenylglycine (Phg), and cyclohexylalanine (Cha), norleucine (Nle), cysteic acid (Cya) and methionine sulfoxide (MSO). These also fall conveniently into particular categories.

Based on the above definition,
Sar and β -ala are neutral/non-polar/small;
t-BuA, t-BuG, N-MeIle, Nle and Cha are neutral/non-polar/large/nonaromatic;

Orn is basic/noncyclic;
Cya is acidic;
Cit, Acetyl Lys, and MSO are neutral/polar/large/nonaromatic; and

Phg is neutral/non-polar/large/aromatic.

Both L and D isomers of amino acids encoded by the genetic code or otherwise are included as amino acids useful in this invention provided the resulting protein processes the required activity.

The various omega-amino acids are classified according to size as neutral/non-polar/small (β -ala, i.e., 3-aminopropionic, 4-aminobutyric) or large (all others).

The nomenclature used to describe compounds of the present invention follows the conventional practice wherein the amino group is assumed to the left and the carboxyl group to the right of each amino acid in the peptide. In the formulas representing selected specific

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embodiments of the present invention, the amino- and carboxyl-terminal groups, although often not specifically shown, will be understood to be in the form they would assume at physiological pH values, unless otherwise specified. Thus, the N-terminal H^+ and C-terminal- O^- at physiological pH are understood to be present though not necessarily specified and shown, either in specific examples or in generic formulas.

Serine Proteases and their Inhibitors (Serpins)

Although originally named for their mechanism of action, members of the serine protease family also show significant sequence and structural homology. Some serine proteases are very specific, cleaving only certain peptide bonds of a specific target protein while others are very nonspecific, degrading multiple target proteins into small peptides.

Serine proteases are regulated at many levels. Some are synthesized as inactive proenzymes and are activated only during specific events and at specific locations. This allows the body to respond rapidly to a physiological perturbation by activating an already present reservoir of proteolytic activity. Coagulation, for example, is carried out when circulating proenzymes such as Factor X and prothrombin are sequentially activated in response to injury resulting in a cascade of clotting activity. In addition, proteolytic activity is often localized to specific sites, such as receptor binding sites which can cause high local concentrations of protease or proenzyme ready for activation.

Once activated, it is extremely important that proteolytic activity be confined both spatially and temporally. This control is often achieved by the presence of specific inhibitors which block proteolytic activity. An important family of related proteins, the

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serine protease inhibitors, or "serpins", are key in the regulation of serine proteases. Like the serine proteases, serpins were first defined by their common mechanism of action but later turned out to be highly homologous both in terms of sequence and structure.

Serpins all contain an inhibitor domain with a reactive peptide bond defined on either side by the variables P_1 and P_1' . In a direction to the left away from the reactive site, the amino acids are referred to as P_1 , P_2 , P_3 , etc., and in a direction to the right away from the reactive site they are referred to as P_1' , P_2' , P_3' , etc. The P_1 residue is recognized by the substrate binding pocket of the target protease which attacks the reactive peptide bond as though a normal substrate.

However, hydrolysis of the peptide bond and release of the protease does not proceed to completion. The normal deacylation step is so slow that the reaction becomes essentially irreversible and the protease becomes trapped in a stable, equimolar complex.

Protease nexin-1 (PN-1) is a member of the serpin family. PN-1 is produced by many different cell types including fibroblasts, glial cells, platelets and microphages. PN-1 is secreted by cells into the extracellular environment where it binds to and inhibits target serine proteases. PN-1-protease complexes then bind back to specific cell surface receptors where they are internalized and degraded.

PN-1 is very similar, both structurally and functionally to antithrombin (AT-III). AT-III is the primary plasma inhibitor of blood coagulation. The inhibition of thrombin by AT-III in plasma is normally very weak but is accelerated significantly by the presence of heparin or by other mucopolysaccharides on the endothelial lining of blood vessels. The therapeutic value of heparin as a blood "thinning" agent is due to

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its enhancement of AT-III activity. Like AT-III, PN-1 has a high affinity heparin binding site and inhibits thrombin much more rapidly (50-100 fold) in the presence of heparin. Thus PN-1 has therapeutic potential as an
5 anticoagulant.

On the other hand, PN-1 differs from AT-III in a number of ways. Unlike AT-III, PN-1 is also a good inhibitor of the fibrinolytic enzymes urokinase and plasmin, as well as trypsin. Furthermore, PN-1 is not
10 found in significant quantities in plasma and may function primarily in the tissues. The high affinity heparin binding site of PN-1 serves to localize it to connective tissues and cells which contain sulfated proteoglycans on their surface and surrounding
15 extracellular matrix. Thus PN-1's primary role seems to be in regulating proteolytic activity in tissues as opposed to blood. Further evidence for the role of PN-1 is found by the fact that it is present in brain tissue and may be involved in peripheral nerve regeneration and
20 neurite extension.

The relative efficiency with which PN-1 inhibits serine proteases can be measured by the second order association rate constant (k_{ass}) as previously described in Bieth, J.G. (Bull. Euro. Physiopath. Resp. (1980)
25 16:183-195), and reported by Scott et al. (J. Biol. Chem. (1985) 260:7029-7034), both of which are incorporated herein by reference to disclose and explain the meaning of the rate association constant. In general, a value for k_{ass} equal to or greater than $1 \times 10^5 \text{ M}^{-1}\text{S}^{-1}$ for a
30 particular protease-inhibitor reaction is considered to be physiologically significant (Travis and Salveson Ann. Rev. Biochem. (1983) 52:655-709). The k_{ass} or rate association constant has inverse-mole-seconds as its units, and the larger the k_{ass} , the more rapid the
35 inhibition. Accordingly, a k_{ass} value is always given as a

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value with respect to a particular enzyme and is zero if there is no inhibition of the enzyme.

Many physiologically important protease inhibitor reactions such as elastase- α -1 antitrypsin and plasmin-
5 α -2-antiplasmin occur with rate constants as high as $1 \times 10^7 \text{ M}^{-1}\text{s}^{-1}$ or greater. The thrombin-PN-1 reaction occurs at a similar high rate in the presence of heparin.

Description of PN-1 (α and β)

Figures 1 and 2, respectively, show the amino acid
10 sequence of PN-1 α and PN-1 β . The α and β forms differ by the substitution of thr₃₁₀-gly₃₁₁ in PN-1 β for arg₃₁₀ in PN-1 α . Alignment of the reactive site center of PN-1 with other serpins, such as antithrombin III, predicts that arginine 345 (346 for PN-1 β) is the reactive site
15 center or "P₁" site. The "P₁" site (arginine at position 345 for PN-1 α and 346 for PN-1 β) has been confirmed by sequencing of the peptide fragment released from PN-1 upon dissociation of complexes with thrombin.
Furthermore, PN-1 normally inhibits only enzymes which
20 cleave at arginine (the P₁ residue), such as thrombin, plasmin, trypsin, plasminogen activators, and plasma kallikrein.

Based on the above and by referring to the sequences of PN-1 α and PN-1 β shown in Figures 1 and 2
25 respectively, it can be seen that the "P₁" site is serine at position 346 for PN-1 α and serine at position 347 for PN-1 β .

Description of Protease Inhibitor Action

In order to allow the body to respond rapidly,
30 several serine proteases are synthesized at relatively high levels in their inactive proenzyme forms and are only activated during specific events. For example, coagulation is carried out when circulating proenzymes

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such as Factor X and prothrombin are sequentially activated in response to an injury. This activation results in a cascade of clotting activity. Proteolytic activity is often localized to specific sites such as
5 receptor binding sites. Once a proteolytic enzyme is activated, it is extremely important that the enzyme activity be confined both spatially and temporally. Such confinement is in part brought about by the inhibitory effect of serpins.

10 All serpins contain an inhibitor domain with a reactive peptide bond defined on either side by P_1 and P_1' residues. The P_1 residue (such as arginine at position 345 for PN-1 α and 346 for PN-1 β) is recognized by the substrate binding pocket of the target protease. Upon
15 recognition of the "reactive" site (of the inhibitor by the protease) the protease attacks the reactive peptide bond of the inhibitor as if it were a normal substrate. However, in the case of serpin hydrolysis of the peptide bond and release of the protease does not proceed to
20 completion. The normal deacylation step is so slow that the reaction becomes essentially irreversible and the protease becomes trapped with the inhibitors in a stable, covalent, equal molar complex. Since the P_1 residue is the predominant determinant residue recognized by the
25 substrate binding pocket of the target protease, alteration of this residue can alter the protease specificity of the inhibitor entirely or substantially change the degree of the inhibitory effect obtainable. Residues near the P_1 residue (i.e., P_4 - P_4') also
30 contribute to protease specificity. Accordingly, alteration of these residues can also lead to modified inhibitory effects.

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Variants in General

Amino acid sequences, active sites and biochemical activity of a number of natural proteins and in particular natural serpins are known. It is also known
5 that some proteins have a high degree of activity with respect to a certain protease, whereas another protein will have virtually no activity with respect to that protease. The present inventors noted this information and deduced that it might be possible to change the
10 protease inhibitory activity of a particular protein, in a directed manner, by replacing its active site with the active site of another protein having a completely different activity with respect to that protease. Alternatively, one can create a variant of the invention
15 by attaching to a first protein, the receptor binding region of a second protein. In that the biochemical function and protein binding specificity of different proteins are known, the methodology of the present invention makes it possible to make certain logical
20 deductions and create a specific variant with a relatively high expectation of not only changing the activity (e.g. binding affinity) of the protein, but changing it in a specific and directed manner.

An example of producing chimeras (Type V variants)
25 of the invention can be carried out as follows. A first protein might be known to have virtually no binding affinity with respect to a given receptor and a second protein might have very high binding affinity with respect to that receptor. (A receptor can be any protein
30 or a portion thereof, ligand, cell surface area or molecule.) By attaching the binding region of the second protein to the first protein one can provide a variant with the biochemical functions of the first protein which will bind to the receptor previously bound only by the
35 second protein. A specific example of utilizing the

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methodology of the present invention in order to take advantage of the binding specificity and biochemical activity of two different proteins is described below.

A specific situation to which variants of the invention might be applied is as follows. The movement of monocytes and neutrophils from the bloodstream into inflamed tissue requires activation events at the site of interaction. These events include expression of adhesion molecules and recruitment of transmigration machinery. To migrate through the endothelium, the connections between the cells must be degraded, including the basement membrane and extracellular matrix. It is now clearly established that the urokinase-type plasminogen activator (uPA)-plasmin system plays a major role in regulating extracellular proteolysis i.e. uPA-plasmin is important in breaking intracellular connections so that neutrophils can migrate through the endothelium blood vessel lining into surrounding tissues. Although the migration of some neutrophils cells through the endothelium to the surrounding tissue is desirable, too much migration too quickly results in undesirable inflammation of the tissue and, possibly, blockage of the bloodstream passing through the inflamed tissues. A variant which would (1) bind to activated endothelium cells and (2) inhibit uPA-plasmin would be useful in preventing and/or reducing inflammation at a particular site.

Tumor cell invasiveness is also dependent upon the uPA-plasmin system as shown in tumor cell metastasis model systems (Ossowski and Reich, 1983; Hearing, et al., 1988) and extracellular matrix degradation and basement membrane invasion (Gergman, et al., 1986; Mignatti, et al., 1986; Reich, et al., 1988; Cajot, et al, 1990). The levels of uPA are significantly higher in human breast cancer tissues than in normal tissues. Increased amounts

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of uPAR correlate with increased invasiveness of malignant cells in model systems (Ossowski, 1988; Hearing, et al., 1988). Agents which block the proteolytic activity of uPA or plasmin may protect
5 against extracellular matrix degradation and basement membrane invasion and aid in preventing inflammation. Similarly, agents which block the interaction of urokinase with the urokinase receptor (uPAR) might block metastasis.

10 A variant protein of the present invention could be designed to block the urokinase receptor and inhibit urokinase. Specifically, a variant could be produced which combined the ability to block the urokinase receptor with the ability to inhibit urokinase and
15 plasmin, and thereby have an effect on alleviating or preventing inflammation. Such a variant would be more effective in reducing or preventing inflammation than would either protein by itself. By making use of the urokinase receptor binding ability of the variant, the
20 variant will localize to the desired specific site of extracellular matrix degradation, specifically preventing further degradation by inhibiting enzymes and preventing the binding of enzymes which cause degradation, thereby having a dual effect on alleviating or preventing
25 inflammation.

To produce a chimeric protein of the present invention the central role of uPA and uPAR in cancer invasion and inflammation were recognized. With this information in mind it was understood that the present
30 invention should provide a chimeric protein which would interfere with the binding of uPA to uPAR and inhibit both uPA and plasmin generated at sites of cellular invasion.

The receptor binding region of uPA has been
35 localized to the 135 residue amino-terminal fragment

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(ATF). This region (i.e. ATF) binds to the uPAR with high affinity (K_d 0.1 to 1 nM) and can competitively inhibit the binding of uPA to the uPAR.

PN-1 blocks tumor cell-mediated extracellular matrix degradation and tumor cell migration in vitro, in that PN-1 inhibits the uPA-plasmin system. In order to generate a more effective and specific inhibitor of tumor metastasis and leukocyte invasion, the present invention provides a chimeric protein consisting of the amino-terminal fragment of uPA and PN-1 (ATF-PN1). Due to the presence of the ATF portion, this chimeric protein has a high affinity to sites of cellular invasion; and due to the PN-1 protein it inhibits uPA and plasmin.

Type I Variant

This aspect of the invention involves the manipulation of the amino acid sequence of the PN-1, so that the reactive site is in some way altered, to change the protease specificity or the degree of inhibitory effect of PN-1 on serine proteases. More specially, the present invention involves substituting one or more amino acids within protease nexin-1 and/or deleting or adding amino acids to the sequence of protease nexin-1 in order to obtain an effect on the reactive site of protease nexin-1 so that the protease specificity of protease nexin-1 and/or the degree of inhibitory effect of protease nexin-1 on a serine protease is changed. In general, the change in protease specificity or degree of inhibitory effect is obtained by substituting an amino acid at the P_1 , P_2 , P_3 , P_4 or, alternatively, P_1' , P_2' , P_3' , P_4' sites. Still more specifically, the invention involves substituting one or both of the " P_1 " site arginine residue or " P_1' " site serine residue with a different residue resulting in PN-1 variants with

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radically different protease specificities and/or inhibitory effects on particular serine proteases.

The PN-1 variants of the invention can also be described in terms of their functionality. Importantly, 5 some of the PN-1 variants of the invention are capable of inhibiting elastase. Within this general group are PN-1 variants wherein the ability to inhibit elastase is greatly enhanced in the presence of heparin and/or heparin-like compounds. Another group of PN-1 variants 10 of the invention include PN-1 variants which have an enhanced ability to inhibit serine proteases as compared with PN-1. The PN-1 variants of the invention are designed to inhibit serine proteases such as urokinase, Factor Xa plasmin, kallikrein, Factor XIIa, Factor XIa, 15 Factor Va, tPA, elastase, cathepsin and contrapsin. Functional objectives of the invention, such as the production of a compounds which inhibit serine proteases such as elastase and whose ability to inhibit such is enhanced in the presence of other compounds such as 20 heparin, are obtained, in general, by manipulating DNA. Specifically, the DNA encoding an enzyme is manipulated by including within the DNA a sequence of DNA which encodes a substrate for a particular serine protease. The recombinant DNA is then expressed to produce a 25 variant of the invention which will include a substrate for the particular serine protease. In that the substrate is present, the activity of that serine protease can be specifically inhibited by the variant while the variant maintains its natural biological 30 activity.

The five different types of variants of the invention will now be described in further detail.

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PN-1 Variants -- Active Site Manipulation

For purposes of clarity, substitution at a single site will be discussed first (P_1 site then P_1' site) followed by a discussion of multiple substitutions.

5 Type I Variants: Single Site Mutations

The arginine residue is a polar, basic amino acid. Substitution of the polar arginine with a non-polar residue has a dramatic effect on the degree of serine protease inhibition obtainable. As a specific example of
10 this effect, reference is made to our compound NCY2010 wherein arginine (at position 345 for α , 346 for β) is substituted with isoleucine (R345I). The R345I variant (i.e., isoleucine has been substituted for arginine a position 345 of PN-1 α) essentially eliminates thrombin
15 inhibitory activity with or without heparin. At the same time, the NCY2010 variant is a good inhibitor of neutrophil elastase activity. This is surprising when it is noted that native fibroblast PN-1 has no inhibitory effect on elastase, and in fact is a substrate for
20 elastase.

The activity of NCY2010 should be viewed with the understanding that the relative efficiency at which protease inhibitors (such as the PN-1 variants of the invention) inhibit serine proteases are measured by a
25 known standard. That standard is the second order association rate constant (k_{ass}) as described in (Bieth, J.G., Bull. Euro. Physiopath. Resp. (1980) 16:183-195) and reported by Scott et al. (J. Biol. Chem. (1985) 260:7029-7034), both of which are incorporated herein by
30 reference to disclose second order association rate constants.

In general, a value for k_{ass} equal to or greater than $1 \times 10^5 \text{ M}^{-1}\text{s}^{-1}$ for a particular protease-inhibitor reaction is considered to be physiologically significant

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(Travis and Salveson Ann. Rev. Biochem. (1983)
52:655-709), incorporated herein by reference to describe
the significance of rate constants. Many physiologically
important protease-inhibitor reactions such as elastase-
5 α -1-antitrypsin and plasmin- α -2-antiplasmin occur with
rate constants as high as $1 \times 10^7 \text{ M}^{-1}\text{S}^{-1}$ or greater. The
thrombin-PN-1 reaction occurs at a similar high rate, or
faster, in the presence of heparin.

Native PN-1 has essentially no effect with respect
10 to inhibiting the activity of elastase. However, the
R345I variants of the present invention clearly provide
not just a new biological activity for the serpin, i.e.,
its ability to inhibit elastase, but clearly provide an
extremely potent elastase inhibitor. The ability of the
15 R345I variants to inhibit elastase to such a degree was
in itself a surprising finding. However, it was clearly
unexpected to find that, in addition to providing such a
potent elastase inhibitor, these variants had still
further increased potency with respect to inhibiting
20 elastase while in the presence of heparin.

Variants of the invention are clearly capable not
only of providing improved potency with respect to acting
as elastase inhibitors, but of providing such activity
site-specifically in that their activity is greatly
25 enhanced in the presence of heparin, heparin-like
compounds or other related mucopolysaccharides normally
found in the endothelial lining of blood vessels. In
addition to heparin, a range of sulfated proteoglycans
such as other heparin-like compounds normally found on
30 the surface and surrounding extracellular matrix would
provide not only increased potency with respect to the
ability of the variants of the invention to inhibit
elastase but provide site-specific activity due to the
affinity of these variants to heparin and heparin-like
35 compounds.

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The inhibitory effect of the R345I variant on elastase is increased approximately two orders of magnitude in the presence of heparin. It can be readily determined that "P₁" variants with non-polar residues such as valine substituted for the polar arginine residue could be used as a heparin activatable inhibitor in order to treat individuals suffering from elastase-related diseases such as emphysema, congenital α -1-antitrypsin deficiency, inflammation and septic shock. Non-polar residues which can be used include G, A, V, L, I, M, F and W, and more preferably (due to "R" group structures similar to valine) G, A, V and L, and most preferably I.

In a broad sense, the present invention encompasses PN-1 variants which are capable of acting as potent elastase inhibitors. More specifically, the invention encompasses such PN-1 variants which act as elastase inhibitors and further wherein the ability to inhibit elastase is greatly increased in the presence of heparin and heparin-like materials. Still more specifically, the invention encompasses PN-1 variants which act as elastase inhibitors and which variants have their ability to inhibit elastase increased 10 fold or more in the presence of heparin, preferably 50 fold or more in the presence of heparin and more preferably 100 fold or more in the presence of heparin. Useful formulations of the invention include PN-1 variants formulated in pharmaceutical compositions along with heparin and heparin-like compounds such as various sulfated polysaccharides or proteoglycans. It is particularly preferred if the heparin-like compounds are highly sulfated, thus providing high negative charges.

Above it has been pointed out that P₁ variants of the invention which include non-polar residues such as valine substituted for the polar arginine can be used to treat individuals due to the ability of these P₁ variants

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to inhibit the activity of elastase. This is quite surprising since other proteases such as urokinase and plasmin which are inhibited by PN-1 are not heparin activatable. While not wishing to be bound by any particular theory, it may be that the P₁ variants of the present invention are effective in inhibiting elastase due to the cationicity of elastase which promotes its binding to heparin which is anionic. Accordingly, in order to obtain other PN-1 variants which are heparin activatable inhibitors of elastase, the active site should be substituted with other residues which are non-polar and have similar "R" groups in order to have a reasonable expectation of similar activity.

Novel Aspects of PN-1 Variants

The sequence of PN-1 α and PN-1 β are given in Figures 1 and 2 respectively. Further, factors describing the characteristics of both have been put forth above. Prior to the present disclosure, variants of the invention such as elastase inhibitors of any PN-1 were not known. Further, it was not known whether any such variants would provide any activity, let alone the type of activity obtained. In fact, elastase cleaves native PN-1. This cleavage inactivates PN-1 toward thrombin and other proteases. It was quite possible that, in changing Arg₃₄₅ to Ile(R345I), PN-1 could be changed into an even better substrate for elastase, leading to even quicker inactivation of PN-1. The present invention not only provides variants wherein active sites have been replaced, but shows that such variants have activity and that the activity is substantially different from the activity of the original PN-1. Now that a number of variants and their activity have been shown, it can be seen that still other variants which might possess activity can also be produced. In

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connection therewith, it is postulated that variants can be produced wherein substitution is made at both the P_1 and P_1' sites. Such double substitutions could be put forth in a variety of different ways.

5 One approach to producing such variants is to substitute one of the sites with a residue which is substantially different from the residue present such as including a non-polar residue in place of a polar residue while substituting the other site with a residue which is
10 substantially similar to the residue present there both in terms of being polar or non-polar and in terms of having a similar "R" group. Another approach is to substitute both sites with residues which are substantially different from the original residues. Yet
15 another possible means for producing variants would be to use either of the above-suggested strategies in combination with substituting other sites. A variety of such substitutions will occur to those skilled in the art upon reading this disclosure. What is important is that
20 the resulting variant continued to provide activity. The ability of the variant to provide activity will depend on the substrate specificity. Accordingly, the present invention is intended to encompass single, double and multiple substitutions of the residues to provide
25 variants which continue to have activity with respect to a given protease or gain substantial activity with respect to another protease.

In connection with the present invention, the PN-1 variants which have activity are variants which have
30 (1) substantially increased potency with respect to inhibiting tPA, urokinase, and/or other related enzymes;
(2) substantially increased potency with respect to inhibiting elastase; or most preferably (3) substantially increased potency with respect to inhibiting elastase and
35 which potency is still further increased dramatically in

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the presence of heparin. In that the present invention has demonstrated that it is possible to produce PN-1 variants which inhibit elastase and has further demonstrated that it is possible to produce such variants
5 which not only inhibit elastase, but have substantially increased potency to inhibit elastase in the presence of heparin others skilled in the art of such inhibitors will be able to deduce other variants which are intended to be within the scope of the present invention.

10 Specific PN-1 Variants

Examples of protease nexin-1 variants of the invention are listed in Table 2 along with "indication" of the variant.

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TABLE 1

<u>Record #</u>	<u>NCY</u>	<u>mutation</u>	<u>sequence</u>	<u>indication</u>
	1	NCY2000	CHO PN-1	TTAILIAR--SSPP
	2	NCY2001	P1Ala	
5	3	NCY2002	P1Arg (WT)	
	4	NCY2003	P1Asn	
	5	NCY2004	P1Asp	
	6	NCY2005	P1Cys	
	7	NCY2006	P1Gln	
10	8	NCY2007	P1Glu	
	9	NCY2008	P1Gly	
	10	NCY2009	P1His	
	11	NCY2010	P1Ile	antielastase
	12	NCY2011	P1Leu	antielastase
15	13	NCY2012	P1Lys	antiplasmin
	14	NCY2013	P1Met	
	15	NCY2014	P1Phe	
	16	NCY2015	P1Pro	
	17	NCY2016	P1Ser	
20	18	NCY2017	P1Thr	
	19	NCY2018	P1Trp	
	20	NCY2019	P1Tyr	
	21	NCY2020	P1Val	antielastase
	22	NCY2021	P2Ala (WT)	
25	23	NCY2022	P2Arg	
	24	NCY2023	P2Asn	
	25	NCY2024	P2Asp	
	26	NCY2025	P2Cys	
	27	NCY2026	P2Gln	
30	28	NCY2027	P2Glu	
	29	NCY2028	P2Gly	faster kinetics
	30	NCY2029	P2His	
	31	NCY2030	P2Ile	
35	32	NCY2031	P2Leu	
	33	NCY2032	P2Lys	
	34	NCY2033	P2Met	
	35	NCY2034	P2Phe	
	36	NCY2035	P2Pro	faster kinetics
40	37	NCY2036	P2Ser	
	38	NCY2037	P2Thr	
	39	NCY2038	P2Trp	
	40	NCY2039	P2Tyr	
45	41	NCY2040	P2Val	
	42	NCY2041	P3Ala	
	43	NCY2042	P3Arg	
	44	NCY2043	P3Asn	
	45	NCY2044	P3Asp	
50	46	NCY2045	P3Cys	
	47	NCY2046	P3Gln	

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<u>Record #</u>	<u>NCY</u>	<u>mutation</u>	<u>sequence</u>	<u>indication</u>
	48	NCY2047	P3Glu	
	49	NCY2048	P3Gly	
	50	NCY2049	P3His	
5	51	NCY2050	P3Ile (WT)	
	52	NCY2051	P3Leu	
	53	NCY2052	P3Lys	
	54	NCY2053	P3Met	
	55	NCY2054	P3Phe	
10	56	NCY2055	P3Pro	
	57	NCY2056	P3Ser	
	58	NCY2057	P3Thr	
	59	NCY2058	P3Trp	
	60	NCY2059	P3Tyr	
15	61	NCY2060	P3Val	
	62	NCY2101	P1'Ala	
	63	NCY2102	P1'Arg	
	64	NCY2103	P1'Asn	
	65	NCY2104	P1'Asp	
20	66	NCY2105	P1'Cys	
	67	NCY2106	P1'Gln	
	68	NCY2107	P1'Glu	
	69	NCY2108	P1'Gly	
	70	NCY2109	P1'His	
25	71	NCY2110	P1'Ile	anti- Factor Xa
	72	NCY2111	P1'Leu	
	73	NCY2112	P1'Lys	
	74	NCY2113	P1'Met	
30	75	NCY2114	P1'Phe	
	76	NCY2115	P1'Pro	
	77	NCY2116	P1'Ser (WT)	
	78	NCY2117	P1'Thr	anti- Factor Xa
35	79	NCY2118	P1'Trp	
	80	NCY2119	P1'Tyr	
	81	NCY2120	P1'Val	

The above examples 1-81 represent the substitution at different sites within the active site of PN-1. For example, record nos. 2-21 represent a substitution at the P₁ position of PN-1. The indication "WT" is provided to indicate the naturally-occurring or wild-type sequence produce via CHO cells. As is evident from this disclosure, the examples could be continued to include all 20 amino acid substitutions at each position within the active site, that is, all 20 naturally-occurring

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amino acids could be substituted, using site-directed mutagenesis, at positions P₁, P₂, P₃, P₄, P₁', P₂', P₃', and P₄'.

It is possible to produce individual type I variants using site-directed mutagenesis. However, it is also possible to produce large numbers of Type I variants at the same time. For example, it is possible to produce the 64 million different variants simultaneously wherein all of the 20 naturally occurring amino acids are substituted at all 8 positions. Such can be carried out using a phage display synthesis methodology as disclosed within U.S. patent 5,223,409 issued June 29, 1993. Further, the chemical synthesis methodology disclosed within U.S. patent 5,010,175 issued April 23, 1991 can be used to produce such large mixtures of variants. Different types of screening methodology such as that disclosed within U.S. patent 5,223,409 can then be used to screen the variants to determine particular activities.

20 Testing Type I Variants

Any of the variants of the present invention can be tested by comparing the variants with a panel of proteases and determining their second-order rate constants with respect to the different proteases. Such tests have been carried out with an exemplary number of Type I variants, and the results are described below in Tables 1A through 1I.

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TABLE 1A
Wild-type (CHO PN-1)
NCY 2000

		<u>Second Order Rate Constant ($M^{-1}s^{-1}$)</u>
5	<u>Protease</u>	
	1) Thrombin	5.98×10^5
	2) Plasmin	1.28×10^5
	3) Plasmin (hp)	4.51×10^5
	4) Xa	7.45×10^3
10	5) Xa (hp)	4.85×10^4
	6) Urokinase	1.49×10^5
	7) Urokinase (hp)	3.30×10^5
	8) Kallikrein	2.50×10^5
	9) Cathepsin G	<100
15	10) Activated protein C	1.42×10^4
	11) Activated protein C (hp)	1.96×10^6
	12) Elastase	<100

(hp) indicates in the presence of 10 $\mu g/ml$ of heparin.

20

TABLE 1B
(E. coli PN-1)
NCY 2002

	<u>Protease</u>	<u>Second Order Rate Constant ($M^{-1}s^{-1}$)</u>
25	1) Thrombin	5.99×10^5
	2) Plasmin	3.44×10^5
	3) Plasmin (hp)	3.98×10^5
	4) Xa	4.82×10^3
	5) Xa (hp)	2.48×10^4
30	6) Urokinase	2.41×10^5
	7) Urokinase (hp)	2.35×10^5
	8) Kallikrein	6.30×10^4
	9) Cathepsin G	<100
	10) Activated protein C	8.56×10^2
35	11) Activated protein C (hp)	2.00×10^5
	12) Elastase	<100

(hp) indicates in the presence of 10 $\mu g/ml$ of heparin.

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TABLE 1C
PN-1 (P₂Gly)
NCY 2028

		<u>Second Order Rate</u> <u>Constant (M⁻¹S⁻¹)</u>
5	<u>Protease</u>	
	1) Thrombin	5.32 x 10 ⁴
	2) Plasmin	5.52 x 10 ⁴
	3) Plasmin (hp)	6.75 x 10 ⁴
	4) Xa	9.43 x 10 ³
10	5) Xa (hp)	5.54 x 10 ⁴
	6) Urokinase	1.13 x 10 ⁵
	7) Urokinase (hp)	<100
	8) Kallikrein	3.24 x 10 ⁴
	9) Cathepsin G	<100
15	10) Activated protein C	<100
	11) Activated protein C (hp)	1.61 x 10 ⁵
	12) Elastase	----

(hp) indicates in the presence of 10 µg/ml of heparin.

20

TABLE 1D
PN-1 (P₂Pro)
NCY 2035

	<u>Protease</u>	<u>Second Order Rate</u> <u>Constant (M⁻¹S⁻¹)</u>
25	1) Thrombin	1.92 x 10 ⁴
	2) Plasmin	8.48 x 10 ³
	3) Plasmin (hp)	1.58 x 10 ⁴
	4) Xa	1.41 x 10 ²
	5) Xa (hp)	7.33 x 10 ²
30	6) Urokinase	<100
	7) Urokinase (hp)	<100
	8) Kallikrein	<100
	9) Cathepsin G	<100
	10) Activated protein C	<100
35	11) Activated protein C (hp)	1.39 x 10 ⁵
	12) Elastase	----

(hp) indicates in the presence of 10 µg/ml of heparin.

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TABLE 1E
PN-1 (P,Val)
NCY 2020

		<u>Second Order Rate</u> <u>Constant ($M^{-1}S^{-1}$)</u>
5	<u>Protease</u>	
	1) Thrombin	<100
	2) Plasmin	----
	3) Plasmin (hp)	----
	4) Xa	----
10	5) Xa (hp)	----
	6) Urokinase	----
	7) Urokinase (hp)	----
	8) Kallikrein	<100
	9) Cathepsin G	<100
15	10) Activated protein C	----
	11) Activated protein C (hp)	----
	12) Elastase	1.20×10^6

(hp) indicates in the presence of 10 μ g/ml of heparin.

20 TABLE 1F
PN-1 (P,Ile)
NCY 2010

	<u>Protease</u>	<u>Second Order Rate</u> <u>Constant ($M^{-1}S^{-1}$)</u>
25	1) Thrombin	<100
	2) Plasmin	----
	3) Plasmin (hp)	----
	4) Xa	----
	5) Xa (hp)	----
30	6) Urokinase	----
	7) Urokinase (hp)	----
	8) Kallikrein	<100
	9) Cathepsin G	<100
	10) Activated protein C	----
35	11) Activated protein C (hp)	----
	12) Elastase	4.15×10^6

(hp) indicates in the presence of 10 μ g/ml of heparin.

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TABLE 1G
PN-1 (P₁Leu)
NCY 2011

		<u>Second Order Rate</u> <u>Constant (M⁻¹S⁻¹)</u>
5	<u>Protease</u>	
	1) Thrombin	<100
	2) Plasmin	----
	3) Plasmin (hp)	----
	4) Xa	----
10	5) Xa (hp)	----
	6) Urokinase	----
	7) Urokinase (hp)	----
	8) Kallikrein	<100
	9) Cathepsin G	<100
15	10) Activated protein C	----
	11) Activated protein C (hp)	----
	12) Elastase	1.65 x 10 ⁶

(hp) indicates in the presence of 10 µg/ml of heparin.

20

TABLE 1H
PN-1 (P₁Lys)
NCY 2012

	<u>Protease</u>	<u>Second Order Rate</u> <u>Constant (M⁻¹S⁻¹)</u>
25	1) Thrombin	2.59 x 10 ⁴
	2) Plasmin	1.01 x 10 ⁵
	3) Plasmin (hp)	1.51 x 10 ⁴
	4) Xa	<100
	5) Xa (hp)	----
30	6) Urokinase	1.16 x 10 ⁴
	7) Urokinase (hp)	----
	8) Kallikrein	<100
	9) Cathepsin G	<100
	10) Activated protein C	<100
35	11) Activated protein C (hp)	3.02 x 10 ⁴
	12) Elastase	----

(hp) indicates in the presence of 10 µg/ml of heparin.

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TABLE 1I
PN-1 (P, Met)
NCY 2013

		<u>Second Order Rate Constant ($M^{-1}S^{-1}$)</u>
5	<u>Protease</u>	
	1) Thrombin	----
	2) Plasmin	----
	3) Plasmin (hp)	----
	4) Xa	----
10	5) Xa (hp)	----
	6) Urokinase	----
	7) Urokinase (hp)	----
	8) Kallikrein	4.81×10^4
	9) Cathepsin G	<100
15	10) Activated protein C	----
	11) Activated protein C (hp)	----
	12) Elastase	<100

(hp) indicates in the presence of 10 μ g/ml of heparin.

20 Type II Variants: Serpin Active Site Swap

Type II variants of the invention are produced in a manner similar to Type I variants. However, the active site of PN-1 is modified in a manner so that it matches the sequence of the active site of another protease, and preferably another serpin. Examples of Type II variants of the present invention include the following:

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TABLE 2

NCY#	Serpin	P ₄	P ₃	P ₂	P ₁	P ₁ '	P ₂ '	P ₃ '	P ₄ '
	Protease Nexin-1	Leu-	Ile-	Ala-	Arg	Ser-	Ser-	Pro-	Pro
5	2203 PAI-1	<u>Val-</u>	<u>Ser-</u>	Ala-	Arg	<u>Met-</u>	<u>Ala-</u>	Pro-	<u>Glu</u>
	2204 PAI-2	<u>Met-</u>	<u>Thr-</u>	<u>Gly-</u>	Arg	<u>Thr-</u>	<u>Gly-</u>	<u>His-</u>	<u>Gly</u> ⊗
	2205 PAI-3*	<u>Phe-</u>	<u>Thr-</u>	<u>Phe-</u>	Arg	Ser-	<u>Ala-</u>	<u>Arg-</u>	<u>Leu</u>
	2201 ATIII	<u>Ile-</u>	<u>Ala-</u>	<u>Gly-</u>	Arg	Ser-	<u>Leu-</u>	<u>Asn-</u>	Pro
10	2206 α ₂ - anti- plasmin	<u>Ala-</u>	<u>Met-</u>	<u>Ser-</u>	Arg	<u>Met-</u>	Ser-	<u>Leu-</u>	<u>Ser</u>
	2207 C1- inhib- itor	<u>Ser-</u>	<u>Val-</u>	Ala-	Arg	<u>Thr-</u>	<u>Leu-</u>	<u>Leu-</u>	<u>Val</u>
15	2208 Kalli- krein BP	<u>Ile-</u>	<u>Leu-</u>	<u>Ser-</u>	Arg	<u>Arg-</u>	<u>Thr-</u>	<u>Ser-</u>	<u>Leu</u> OR
	2209 (rat)	<u>Phe-</u>	<u>Arg-</u>	<u>Ile-</u>	<u>Leu</u>	Ser-	<u>Arg-</u>	<u>Arg-</u>	<u>Thr</u>
	2210 α ₁ AT	<u>Ala-</u>	<u>Ile-</u>	<u>Pro-</u>	<u>Met</u>	Ser-	<u>Ile-</u>	Pro-	Pro
20	2211 α ₁ AT <u>Glu-</u> related	<u>Lys-</u>	Ala-	<u>Trp</u>	Ser-	<u>Lys-</u>	<u>Tyr-</u>	<u>Gln</u>	
	2212 α ₁ AC	<u>Leu-</u>	<u>Leu-</u>	<u>Ser-</u>	<u>Ala</u>	<u>Leu-</u>	<u>Val-</u>	<u>Glu-</u>	<u>Thr</u> OR
		<u>Ile-</u>	<u>Thr-</u>	<u>Leu-</u>	<u>Leu</u>	Ser-	<u>Ala-</u>	<u>Leu-</u>	<u>Val</u>
	2202 HCII	<u>Phe-</u>	<u>Met-</u>	<u>Pro-</u>	<u>Leu</u>	Ser-	<u>Thr-</u>	<u>Glu-</u>	<u>Val</u>
25	2213 uro- kinase inh.	<u>Met-</u>	<u>Thr-</u>	<u>Gly-</u>	Arg	<u>Thr-</u>	<u>Gly-</u>	<u>His-</u>	<u>Gly</u> ⊗

⊗ indicates the sequence is preferably followed by
 30 -Gly-Pro

Underlining residues indicates a difference from the
 natural PN-1 sequence.

This table is meant as an example and should not be
 considered limiting of Type II variants of the invention.

35 The same methodology referred to above with
 respect to Type I variants can be used in the production
 of Type II variants. Further, the methodology disclosed

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within the above-cited patents (incorporated herein by reference) can be used to produce Type II variants. The methodology is modified only by first determining the active site of another serpin. After determining the amino acid sequence of the active site of a different serpin and studying the activity of that different serpin it is possible to produce a Type II variant having a particular and desired changed activity as compared with the naturally occurring PN-1.

10 Testing Type II Variants

As indicated above, all of the variants of the present invention can be tested by determining their second order rate constants relative to a panel of proteases. As with the Type I variants, tests were carried out with a representative number of Type II variants, and the results obtained are put forth below in Tables 2A and 2B.

TABLE 2A
2201 (AT III)

20	<u>Protease</u>	<u>Second Order Rate Constant ($M^{-1}S^{-1}$)</u>
	1) Thrombin	1.69×10^4
	2) Plasmin	2.74×10^4
	3) Plasmin (hp)	4.45×10^4
25	4) Xa	4.21×10^3
	5) Xa (hp)	2.98×10^4
	6) Urokinase	<100
	7) Urokinase (hp)	----
	8) Kallikrein	9.49×10^4
30	9) Cathepsin G	<100
	10) Activated protein C	<100
	11) Activated protein C (hp)	----
	12) Elastase	----

35 (hp) indicates in the presence of 10 $\mu g/ml$ of heparin.

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TABLE 2B
2202 (HC II)

<u>Protease</u>		<u>Second Order Rate</u> <u>Constant (M⁻¹S⁻¹)</u>
5	1) Thrombin	3.36 x 10 ³
	2) Plasmin	<100
	3) Plasmin (hp)	----
	4) Xa	<100
	5) Xa (hp)	----
10	6) Urokinase	<100
	7) Urokinase (hp)	----
	8) Kallikrein	<100
	9) Cathepsin G	4.60 x 10 ⁵
	10) Activated protein C	<100
15	11) Activated protein C (hp)	----
	12) Elastase	<100

(hp) indicates in the presence of 10 µg/ml of heparin.

The activity of NCY 2202 (particularly in the presence of heparin) is analogous in some ways to that of NCY 2322 in that both inhibit cathepsin G but not elastase. This is completely unexpected due to the similar substrate specificity.

Type III Variants: Incorporation of a Substrate Sequence

25 Type III variants of the invention are produced by first determining the substrate sequence of a protease. The substrate sequences of some proteases which are known and which would be useful in connection with the present invention are put forth below in Table 3A.

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TABLE 3A

<u>PROTEASE</u>	<u>substrate sequence</u>
Thrombin	D-Phe-Pip-Arg-pNA Ts-Gly-Pro-Arg-pNA
5 Factor Xa	bz-Ile-Glu(γ OR)-Gly-Arg-pNA cbo-D-Arg-Gly-Arg-pNA
Factor XIa	Glu-Pro-Arg-pNA
Plasmin	(D/L)-Val-Leu-Lys-pNA D-Val-Phe-Lys-pNA Ts-Gly-Pro-Lys-pNA 10 Glu-Phe-Lys-pNA
Urokinase	Glu-Gly-Arg-pNA Bz-Ala-Gly-Arg-pNA
tPA	(D/L)-Ile-Pro-Arg-pNA
15 C1-esterase	z-Val-Gly-Arg-pNA
Kallikrein	(D/Bz)-Pro-Phe-Arg-pNA
Neutrophile elastase	Glu-Pro-Val-pNA Ala-Ala-Pro-Val-pNA
Cathepsin G	Ala-Ala-Pro-Phe-pNA Ala-Ala-Pro-Leu-pNA 20
Pancreatic elastase	Ala-Ala-Ala-pNA

Other substrate sequences can be determined by determining the best artificial small molecule peptide substrates (i.e. Ala-Ala-Pro-Phe-pNA) as determined by k_{cat} and k_{μ} , or by examining the sequence of natural protein substrates (e.g. fibrinogen for thrombin).

After determining the amino acid sequence which a protease will bind to (i.e. its specific substrate sequence), that sequence is used to replace all or a portion of the active site of PN-1. Examples of Type III variants are as follows:

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TABLE 3B

<u>Record #</u>	<u>NCY</u>	<u>mutation</u>	<u>sequence</u>	<u>indication</u>
1	NCY2301	XaS	IEGR--	anticoag.
2	NCY2302	Fibrinogen	DPLAGGGGVR--	thrombin inhibition
5 3	NCY2303	HMWK	SPFR-SVQ	kallikrein inh.
4	NCY2310	FPR	FPR--	thrombin
5	NCY2311	EPV	EPV--	elastase
10 6	NCY2321	AAPF	AAPF	cathepsin G. inh.
7	NCY2322	AAPL	AAPL--	Elastase
8	NCY2323	AAPV	AAPV--	Elastase
9	NCY2324	AAPV	AAPV--	Elastase

15 Testing Type III Variants

In Table 3B above, specific Type III variants are shown. Substrate sequences of proteases such as those shown within Table 3A are included within PN-1. These variants were tested against a panel of proteases, and
 20 the results are shown below in Tables 3C through 3J.

TABLE 3C
2301 (Xa S)

<u>Protease</u>	<u>Second Order Rate Constant (M⁻¹S⁻¹)</u>
25 1) Thrombin	<100
2) Plasmin	2.45 x 10 ⁴
3) Plasmin (hp)	2.54 x 10 ⁴
4) Xa	1.37 x 10 ³
5) Xa (hp)	6.83 x 10 ³
30 6) Urokinase	5.71 x 10 ³
7) Urokinase (hp)	----
8) Kallikrein	<100
9) Cathepsin G	<100
10) Activated protein C	<100
35 11) Activated protein C (hp)	----
12) Elastase	----

(hp) indicates in the presence of 10 µg/ml of heparin.

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TABLE 3D
2303 (HMWK)

<u>Protease</u>		<u>Second Order Rate Constant ($M^{-1}S^{-1}$)</u>
5	1) Thrombin	2.27×10^3
	2) Plasmin	<100
	3) Plasmin (hp)	----
	4) Xa	<100
	5) Xa (hp)	----
10	6) Urokinase	<100
	7) Urokinase (hp)	----
	8) Kallikrein	<100
	9) Cathepsin G	<100
	10) Activated protein C	<100
15	11) Activated protein C (hp)	----
	12) Elastase	----

(hp) indicates in the presence of 10 μ g/ml of heparin.

TABLE 3E
2310 (FPR)

<u>Protease</u>		<u>Second Order Rate Constant ($M^{-1}S^{-1}$)</u>
25	1) Thrombin	4.13×10^4
	2) Plasmin	5.12×10^4
	3) Plasmin (hp)	1.32×10^5
	4) Xa	3.30×10^2
	5) Xa (hp)	----
30	6) Urokinase	5.30×10^3
	7) Urokinase (hp)	----
	8) Kallikrein	<100
	9) Cathepsin G	<100
	10) Activated protein C	<100
35	11) Activated protein C (hp)	4.74×10^5
	12) Elastase	----

(hp) indicates in the presence of 10 μ g/ml of heparin.

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TABLE 3F
2321 (AAPF)

<u>Protease</u>		<u>Second Order Rate Constant ($M^{-1}s^{-1}$)</u>
5	1) Thrombin	7.02×10^3
	2) Plasmin	<100
	3) Plasmin (hp)	----
	4) Xa	<100
	5) Xa (hp)	----
10	6) Urokinase	----
	7) Urokinase (hp)	----
	8) Kallikrein	<100
	9) Cathepsin G	<100
	10) Activated protein C	----
15	11) Activated protein C (hp)	----
	12) Elastase	<100

(hp) indicates in the presence of 10 $\mu g/ml$ of heparin.

TABLE 3G
2322 (AAPL)

<u>Protease</u>		<u>Second Order Rate Constant ($M^{-1}s^{-1}$)</u>
20	1) Thrombin	----
	2) Plasmin	----
	3) Plasmin (hp)	----
	4) Xa	----
	5) Xa (hp)	----
25	6) Urokinase	----
	7) Urokinase (hp)	----
	8) Kallikrein	<100
	9) Cathepsin G	4.0×10^5
	10) Activated protein C	----
30	11) Activated protein C (hp)	----
	12) Elastase	<100

35

(hp) indicates in the presence of 10 $\mu g/ml$ of heparin.

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TABLE 3H
2324 (AAPI)

<u>Protease</u>		<u>Second Order Rate Constant ($M^{-1}s^{-1}$)</u>
5	1) Thrombin	----
	2) Plasmin	----
	3) Plasmin (hp)	----
	4) Xa	----
	5) Xa (hp)	----
10	6) Urokinase	----
	7) Urokinase (hp)	----
	8) Kallikrein	<100
	9) Cathepsin G	<100
	10) Activated protein C	----
15	11) Activated protein C (hp)	----
	12) Elastase	<100

(hp) indicates in the presence of 10 $\mu g/ml$ of heparin.

TABLE 3I
2323 (AAPV)

<u>Protease</u>		<u>Second Order Rate Constant ($M^{-1}s^{-1}$)</u>
25	1) Thrombin	----
	2) Plasmin	----
	3) Plasmin (hp)	----
	4) Xa	----
	5) Xa (hp)	----
30	6) Urokinase	----
	7) Urokinase (hp)	----
	8) Kallikrein	<100
	9) Cathepsin G	<100
	10) Activated protein C	----
35	11) Activated protein C (hp)	----
	12) Elastase	<100

(hp) indicates in the presence of 10 $\mu g/ml$ of heparin.

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TABLE 3J
2311 (EPV)

<u>Protease</u>		<u>Second Order Rate Constant ($M^{-1}s^{-1}$)</u>
5	1) Thrombin	<100
	2) Plasmin	----
	3) Plasmin (hp)	----
	4) Xa	----
	5) Xa (hp)	----
10	6) Urokinase	----
	7) Urokinase (hp)	----
	8) Kallikrein	<100
	9) Cathepsin G	<100
	10) Activated protein C	----
15	11) Activated protein C (hp)	----
	12) Elastase	<100

(hp) indicates in the presence of 10 μ g/ml of heparin.

Type IV Variants

20 The Type IV variants of the invention are quite different from all of the other variants in that the amino acid sequence may be the same as the naturally-occurring protein or different therefrom. Type IV variants may be generated by covalently binding (i.e.,

25 coupling) PEG to any protein, protein fragment, or peptide in general when increased biological stability is desired. Of particular interest are those proteins, protein fragments, and peptides which are useful in therapeutic applications, such as serine protease

30 inhibitor proteins, growth factors, and cytokines. The proteins PN-1, human growth hormone (hGH), erythropoietin (EPO), and antithrombin-III (ATIII) are of particular interest. Specific exemplary proteins of interest, as well as exemplary classes of proteins, which can be

35 modified to create a Type IV variant using the methods of the invention are provided in Table 4A.

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TABLE 4A

Exemplary Proteins and Protein Classes for Generation
of Type IV Variants

SPECIFIC EXEMPLARY PROTEINS	
5	interferon- α 2A
	insulin-like growth factor-1 (IGF-1)
	interferon- α 2B
	insulin
	human growth hormone (hGH)
	transforming growth factor (TGF)
	erythropoietin (EPO)
	ciliary neurite transforming factor (CNTF)
	thrombopoietin (TPO)
	brain-derived neurite factor (BDNF)
10	IL-1
	insulintropin
	IL-2
	glial-derived neurite factor (GDNF)*
	IL-1 RA
	tissue plasminogen activator (tPA)
	superoxide dismutase (SOD)
	urokinase
	catalase
	streptokinase
15	fibroblast growth factor (FGF) (acidic or basic)
	hemoglobin
	neurite growth factor (NGF)
	adenosine deamidase
20	granulocyte macrophage colony stimulating factor (GM-CSF)
	bovine growth hormone (BGH)
	granulocyte colony stimulating factor (G-CSF)
	calcitonin
25	platelet derived growth factor (PDGF)
	bactericidal/permeability increasing protein (BPI)
	L-asparaginase
	arginase
	uricase
	phenylalanine
	γ -interferon
	ammonia lyase

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TABLE 4A (cont.)

EXEMPLARY CLASSES OF PROTEINS	
proteases	pituitary hormones
protease inhibitors	growth factors
5 cytokines	somatomedians
chemokines	immunoglobulins
gonadotrophins	interleukins
chemotactins	interferons
lipid-binding proteins	allergens

10 * GDNF is the same protein as protease nexin-1 (PN-1).

Type IV variants are created by attaching polyethylene glycol to a thio group on a cysteine residue of the protein. The PEG moiety attached to the protein may range in molecular weight from about 200 to
 15 20,000 MW. Preferably the PEG moiety will be from about 1,000 to 8,000 MW, more preferably from about 3,250 to 5,000, most preferably 5,000 MW.

General methods of attaching polyethylene glycol to proteins are disclosed within U.S. Patent 4,179,337
 20 issued December 18, 1979 (incorporated herein by reference to disclose methods of attaching polyethylene glycol to proteins). Further, other methods of attaching polyethylene glycol are disclosed within U.S. Patent 5,122,614 issued June 16, 1992, also incorporated herein
 25 by reference to disclose methods of attaching polyethylene glycol to proteins.

The present inventors have discovered that novel modified proteins can be created by attaching the polyethylene glycol to a cysteine residue within the
 30 protein. Preferably, the protein is modified by attaching the polyethylene glycol to a cysteine residue at a position which is normally glycosylated. In another preferred embodiment, a cysteine residue is added at a

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position which is normally glycosylated (e.g. N-glycosylated), and the polyethylene glycol is attached to the thio group of the added cysteine residue. In addition, if the protein of interest is one member of a family of structurally related proteins, glycosylation sites for any other member can be matched to an amino acid on the protein of interest, and that amino acid changed to cysteine for attachment of the polyethylene glycol. Alternatively, if a crystal structure has been determined for the protein of interest or a related protein, surface residues away from the active site or binding site can be changed to cysteine for the attachment of polyethylene glycol.

It has also been found that it is possible to attach other groups to the thio group of the cysteine residue. For example, the protein may be biotinylated by attaching biotin to a thio group of a cysteine residue. Examples of Type IV variants are as follows:

TABLE 4

<u>Record #</u>	<u>NCY</u>	<u>mutation</u>	<u>sequence</u>	<u>indication</u>
1	NCY2601	PEG-PN1	lys-modified	long half-life
2	NCY2611	Biotin-PN1	lys-modified	detection/coupling
3	NCY2621	PEG-PN1	cys-modified	long half-life
4	NCY2631	Biotin-PN1	cys-modified	detection/coupling

Of the above examples, records numbers 1 and 2 are of a general type known in the art in that the polyethylene glycol or biotin is attached to lysine position of the peptide. However, record numbers 3 and 4 are, respectively, examples wherein the polyethylene glycol or biotin are connected at a cysteine group. The importance of such is described further below.

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The addition of polyethylene glycol (PEG) to proteins is a common method to increase serum half-life and decrease immunogenicity and antigenicity. Nucci et al. describe several proteins which have been modified by addition of PEG including adenosine deamidase, L-asparaginase for treatment of acute lymphoblastic leukemia, interferon alpha 2b (IFN- α 2b) as an anticancer and antiviral drug, superoxide dismutase as an anticancer drug, streptokinase, tPA, urokinase, uricase, hemoglobin, interleukins, interferons, TGF- β , EGF, and other growth factors (Nucci et al., 1991, *Adv. Drug Delivery Rev.* 6:133-151).

Typically, this modification of a protein by attachment of a PEG moiety involves activating PEG with a functional group which will react with lysine residues on the surface of the protein. If the modification of the protein goes to completion, the activity of the protein is usually lost. Current modification procedures allow only partial PEGylation of the protein. Usually this results in only 50% loss of activity and greatly increased serum half-life, so that the overall dose of the protein required for the desired activity is lower.

An unavoidable result of the partial modification is that there will be a statistical distribution of the number of PEG groups per protein, each PEG attached to a lysine residue. Also, there will be a random usage of lysine residues on the surface. For instance, when adenosine deaminase is optimally modified, there is a loss of 50% activity when the protein has about 14 PEG per protein, with a broad distribution of actual PEG per individual protein and a broad distribution of actual lysine residues used.

Early work on PEG modification relied on activating PEG with cyanuric chloride and the coupling with proteins. This approach suffers from several

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disadvantages, most noteworthy are the toxicity of cyanuric chloride and loss of activity. There have been significant advances recently to reduce the toxicity of the chemicals involved in the PEGylation reactions.

5 Zalipsky, et al. (Zalipsky, S., Seltezer, R. & Nho, K. (1991) Polymeric Drugs and Drug Delivery Systems. ACS.) describe the use of succinimydyl carbonates of PEG to produce stable carbamate linkages with proteins via free lysine residues. There are several other methods for
10 modification of proteins with PEG through free lysine residues, but each suffers from the problems associated with partial, random modification of proteins and the potential for losing activity if lysine residues are important.

15 The current state of the art of PEGylation technology could be greatly improved upon if the reaction could be made more specific. For instance, if the reactive region of the protein could be blocked during PEGylation, it is expected that the protein would retain
20 all activity even after saturation modification. This may prove to be expensive and inconvenient (except if the modification took place during an affinity purification step where the active site is protected, and the protein is purified all in one step). In some cases to block the
25 active site region would lead to irrecoverable loss of activity, and so this method could not be employed.

Another alternative is to PEG-modify other residues such as His, Trp, Cys, Asp, Glu, etc. in such a manner that activity is not lost. It is anticipated or
30 likely that many of these residues will be at or near the active site or that these residues will not be at the surface or in sufficient number to significantly affect serum half-life, or that the modification chemistry is not specific enough for the target residue, or the

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chemistry is too harsh for the protein to withstand without loss of activity.

The most desirable situation would be if there were a surface distribution of an amino acid which is
5 reactive and can be modified easily and specifically and is away from the active site region. Cysteine is an ideal candidate for such modification since it is rarely used at or near the active site (except cysteine proteases) and modification chemistry has been well
10 established. Maleimido-PEG is perhaps the most useful, but other chemistries are available for specific cysteine modification. Using site-directed mutagenesis, new cysteine residues can be added on the surface, away from the active site region. This is most conveniently and
15 easily done if a X-ray crystal structure is known.

Even with this protein engineering strategy it is not easily known *a priori* which surface residues to change to cysteine and how many PEG modification sites to add in order to increase stability sufficiently. There
20 are many strategies, among them to create 20 or more independent single-site cysteine mutations, PEGylate each independently and analyze each for remaining activity. Mutant proteins which retain sufficient activity can be combined to generate one protein with multiple PEG
25 attachment sites.

There is another strategy to identify good PEG attachment sites which has the advantage that one does not require knowledge of the three dimensional structure, and also takes advantage of the selective power of
30 evolution to weed out bad sites. Nature has chosen to add glycosylation residues to the surface of secreted proteins to aid stability and increase serum half-life. For example, asparagine residues are glycosylated when part of a well known N-glycosylation signal (NP!T/SP!).
35 Replacement of these Asn residues by cysteine, followed

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by cysteine-specific PEGylation is expected to lead to proteins with significantly increased serum half-life with a minimum loss in activity. To date, this is the closest thing to in vitro glycosylation, and in some
5 respects may be better since glycosylation with inappropriate sugar residues may lead to increased clearance from the serum by the liver, whereas PEG residues are expected to be rather inert.

If a higher degree of PEG modification is desired
10 and the protein to be modified is one member of a family of structurally related proteins, other members of the same family will often have one or more sites of glycosylation not found in the protein of interest. If these "new" potential sites are in a region which is
15 reasonably conserved (i.e. not part of an insertion or with a sequence which is so different that it is likely to have a different structure) it is expected that replacement of the residue equivalent to the Asn with cysteine followed by PEGylation will result in a more
20 highly PEG modified protein without significant loss in activity.

If a further higher degree of PEG modification is required, other solvent accessible residues can be changed to cysteine, and the resultant protein subjected
25 to PEGylation. Appropriate residues can easily be determined by those skilled in the art. For instance, if a three-dimensional structure is available for the protein of interest, or a related protein, solvent accessible amino acids are easily identified. Also,
30 charged amino acids such as Lys, Arg, Asp and Glu are almost exclusively found on the surface of proteins. Substitution of one, two or many of these residues with cysteine will provide additional sites for PEG attachment. In addition, amino acid sequences in the
35 native protein which are recognized by antibodies are

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usually on the surface of the protein. These and other methods for determining solvent accessible amino acids are well known to those skilled in the art.

Modification of proteins with PEG can also be used to generate dimers and multimeric complexes of proteins, fragments, and/or peptides which have increased biological stability potency. These dimeric and multimeric proteins of the invention may be naturally occurring dimeric or multimeric proteins. For example, the dimer or multimer may be composed of cross-linked subunits of a protein (e.g., hemoglobin). Alternatively, the dimeric and multimeric proteins may be composed of two proteins which are not normally cross-linked (e.g., a dimer of cross-linked EPO protein.

Dimeric proteins of the invention may be produced by reacting the protein with (Maleimido)₂-PEG, a reagent composed of PEG having two protein-reactive moieties. This PEGylation reaction with the bi-functional PEG moiety generates dimers of the general formula:



where R₁ and R₂ may represent the same or different proteins and S represents the thio group of a cysteine either present in the native R₁ or R₂ protein, or introduced by site-directed mutagenesis. The proteins R₁ and R₂ may each vary in size from about 6 to 1,000 amino acids, preferably about 20 to 400 amino acids, more preferably 40 to 200 amino acids. In dimeric molecules, R₁ and R₂ are preferably from about 100 to 200 amino acids. Dimers and multimers of particular interest include those composed of proteins, protein fragments and/or peptides which are less than about 40,000 molecular weight.

Where the protein contains (or is engineered to contain) more than one free cysteine, multimeric proteins

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where the proteins (represented by R_1, R_2, \dots, R_n) may be the same or different can be generated. The proteins represented by R_1, R_2, \dots, R_n may vary in size from about 6 to 1,000 amino acids, preferably 20 to 400 amino acids, more preferably 40 to 200 amino acids. Such multimeric proteins may be of the following general formula:



where R_1 represents the protein having multiple free cysteines, for example from 2 to 20 free cysteines, usually from 5 to 7 free cysteines. R_2 may represent a protein the same as or different from R_1 . Furthermore, each of the R_2 proteins attached to R_1 may be the same proteins, or represent several different proteins.

The degree of multimeric cross-linking can be controlled by the number of cysteines either present and/or engineering into the protein and by the concentration of (Maleimido)₂PEG used in the reaction mixture. In addition, the Maleimido-PEG+ (Maleimido)₂-PEG reagents may be used in the same reaction with proteins for formation of couplings of proteins having simple PEG moieties as well as PEG cross-links between proteins within the complex. The dimeric or multimeric protein generated will have an increased half-life relative to the native, protein, due at least in part to its increased size relative to the native protein. Such larger proteins are not degraded or cleared from the circulation by the kidneys as quickly as are smaller proteins. In addition, activity or potency of the dimeric or multimeric protein may be increased.

Dimeric and multimeric proteins may be generated by reaction with Maleimido-PEG or (Maleimido)₂-PEG. Exemplary proteins for dimeric and/or multimeric complex formation using the method of the invention include PN-1, PN-1 variants, hemoglobin, and erythropoietin (EPO), as well as any of the proteins or members of the protein

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classes exemplified in Table 4A. Preferably, the protein generated by the method of the invention is a PEGylated cross-linked complex of the "a" and "b" chains of hemoglobin, multimeric complexes of hemoglobin having
5 intermolecular and/or intramolecular cross-links may also be generated by the subject method.

In general, the method of identifying cysteine residues for PEG modification, and/or identifying amino acid residues to be replaced with cysteine which are
10 subsequently modified by attachment of PEG, provides for generation of a PEGylated protein which can be reasonably expected to retain most or all of the activity of the native protein. The sites selected for modification and/or substitution with cysteine are selected on the
15 basis of the structure of the protein, i.e. the selected sites are solvent accessible residues which are not involved in the active site.

The effect of mutations located outside of the active site are generally predictable in that they
20 generally do not change the primary activity of the protein. In addition, the structural mutations described herein are within solvent-accessible regions of the protein (i.e. on the protein "surface") which have limited or no interaction with other residues in the
25 protein molecule. Thus, mutations at these positions are unlikely to affect the conformation of any other amino acid in a protein.

Type V Variants

Type V variants of the invention are produced by
30 fusing all or a fragment of another protein to PN-1. Preferably, the amino terminal fragment of a protein such as urokinase is fused to PN-1 in order to localize PN-1 to a different receptor, i.e. to the urokinase receptor. In addition to using urokinase, it is possible to fuse

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the amino terminal fragment of proteins such as tPA, Factor IX, Factor X, and Protein C. Examples of Type V variants are as follows:

TABLE 5

5	<u>Record #</u>	<u>NCY</u>	<u>mutation</u>	<u>sequence</u>	<u>indication</u>
	1	NCY2501	ATF-PN1	urokinaseATF	anti-metastasis
	2	NCY2502	HSA-PN1	HSA chimera	long half-life
10	3	NCY2503	IgG-PN1	IgG chimera	long half-life
	4	NCY2504	F9-PN1	Factor IX chimera	anti-coagulation
	5	NCY2505	F10-PN1	Factor X chimera	anti-coagulation
15	6	NCY2506	APC-PN1	Protein C chimera	pro-coagulant

The type V variants of the invention can be produced in manner similar to variants of type I, II and
 20 III. However, it is more preferable to produce such variants by chemically fusing an N-terminal fragment of a different protein to the PN-1.

The Type V variants can also be produced by chemical linkage of purified preparations of both protein
 25 components. Such linkage is conveniently accomplished by using bi-functional cross-linking reagents. Methods for chemically establishing such linkages are well known to those skilled in the art. Specific variants which might be produced in this manner include variants produced by
 30 fusing PN-1 to any one of: EGF; Factor IX; Factor X; and APC.

The method of PEGylation of the invention is intended to be a general procedure and as such is applicable to any protein to increase solubility,
 35 circulating half life and/or to decrease immunogenicity.

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Testing Type V Variants

The Type V variants of the invention are chimeric proteins wherein PN-1 is covalently bound to another protein. The same panel of proteases indicated above
 5 were used to test one of the Type V variants of the invention, and the results are put forth below.

TABLE 5A2501 (ATF-PN-1)

10 <u>Protease</u>	<u>Second Order Rate Constant ($M^{-1}S^{-1}$)</u>
1) Thrombin	5.8×10^5
2) Plasmin	3.5×10^5
3) Plasmin (hp)	----
4) Xa	----
15 5) Xa (hp)	----
6) Urokinase	2.3×10^5
7) Urokinase (hp)	----
8) Kallikrein	----
9) Cathepsin G	----
20 10) Activated protein C	----
11) Activated protein C (hp)	----
12) Elastase	----

(hp) indicates in the presence of 10 $\mu g/ml$ of heparin.

25 Use and Administration

The different chimeric proteins, PN-1 variants, and cysteine-PEGylated proteins of the invention (as indicated above) can provide different effects. For example, P_1 variants with non-polar residues such as
 30 valine substituted for the polar arginine residue could be used as heparin activatable inhibitors. Such inhibitors could be used to treat individuals suffering from elastase-related diseases. Although not limited to such diseases, such variants could be used to treat

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emphysema, congenital α -1-antitrypsin deficiency, inflammation, arthritis and septic shock.

One of the most important and immediate perceived uses of the chimeric proteins, PN-1 variants, and/or
5 cysteine-PEGylated versions of these proteins of the invention is the inclusion of such within various topical formulations such as creams or gels, or a combination of such formulations, with various bandages for application to wounds to aid in wound healing and decrease
10 inflammation at wound sites. In that chimeric proteins, PN-1 variants, and cysteine-PEGylated versions of these proteins of the invention are believed to be effective in decreasing inflammation, injectable formulations containing the chimeric proteins, PN-1 variants, and/or
15 cysteine-PEGylated versions of these proteins of the invention may be injected directly into inflamed joints or other inflamed areas of the body in order to decrease the inflammation. Further the formulations of the invention may be used prophylactically by providing the
20 chimeric proteins, PN-1 variants, and/or cysteine-PEGylated versions of these proteins to a particular site which may be subjected to trauma, (such as in surgery), and thus inflammation, to prevent the inflammation from occurring.

25 Generally, the pharmaceutical compositions containing the chimeric proteins, PN-1 variants, and/or cysteine-PEGylated proteins of the invention will be formulated in a non-toxic, inert, pharmaceutically acceptable aqueous carrier medium, preferably at a pH of
30 about 5 to 8, more preferably 6 to 8, although the preferred pH of the pharmaceutical composition may vary according to the protein employed and condition to be treated.

Of particular interest in the present invention
35 are cysteine-PEGylated proteins and pharmaceutical

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compositions containing these protein. PEGylation of proteins generates proteins which are ready for immediate therapeutic use (i.e. do not require reconstitution), have increased solubility and have an increased half-life and are reduced in immunogenicity and antigenicity relative to the unmodified protein (Nucci et al. 1991 *Adv. Drug Delivery res.* 6:133-151). The increased half-life of PEGylated proteins decreases the amount of protein needed for an effective dosage, reduces the number and frequency of administrations required, and decreases the patient's exposure to the protein, thus decreasing the potential for allergic reactions, toxic effects, or other side effect. These characteristics of PEGylated proteins allow for long-term use of the protein with less potential for undesirable side effects related to protein immunogenicity and/or toxicity. Exemplary proteins for which an increase half-life has effected by PEGylation of the protein include: hGH, insulin, interferon-alpha2A (IFN-alpha-2A), interferon-alpha2B (IFN-alpha-2B), tPA, EPO, G-CSF, antigen E, arginase, asparaginase, adenosine deaminase, batroxobin, bovine serum albumin, catalase, elastase, factor VIII, galactosidase, alpha-galactosidase, beta-glucuronidase, IgG, honeybee venom, hemoglobin, interleukin-2, lipase, phenylalanine ammonia lyase, alpha₁-proteinase inhibitor, pro-urokinase, purine nucleoside phosphorylase, ragweed allergen, streptokinase, superoxide dismutase, tPA, D-alpha-tocopherol, trypsin, tryptophanase, uricase, and urokinase (see in general Nucci et al. *ibid.*; see also Davis et al. 1981 *Clin. Exp. Immunol.* 46:649-652 (bovine adenosine deaminase); Nishimura, et al. 1985 *Life Sci.* 33:1467-1473 (batroxobin); Savoca et al. 1979 *Biochimica et Biophysica ACTA* 578:47-53 (arginase); Till, et al. 1983 *J. Trauma* 23:269-277 (asparaginase); Veronese, et al. 1983 *J. Pharm. Pharmacol.* 35:281-283 (superoxide

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dismutase); Davis et al. 1981 *Lancet* 2:281-283 (urate oxidase); and Dellinger et al. 1976 *Cancer* 38:1843-1846).

PEGylated proteins may be administered for the treatment of a wide variety of diseases. Exemplary disease conditions and the proteins useful in treatment of these diseases are provided in Table 6A.

TABLE 6A
Exemplary Disease Conditions Amenable to Protein Therapy

10	<u>Enzyme Deficiency</u> adenosine deaminase, Purine nucleotide phosphorylase Galactosidase β -glucuronidase	<u>Endotoxic Shock/Sepsis</u> Bactericidal/permeability increasing protein Lipid-binding protein (LBP)
15	<u>Antioxidants for Cancer Therapy</u> Superoxide dismutase Catalase	<u>Blood Protein Replacement Therapy</u> Hemoglobin Albumin
20	<u>Cancer</u> Interferon- α Interferon- γ IL-1- α Phenylalanine ammonia lyase Arginase L-asparaginase	<u>Growth Factors (for use in wound healing, induction of red blood cell formation, etc.)</u> Epidermal growth factor G-CSF Interferon- γ Transforming growth factor
25	Uricase Granulocyte colony stimulating factor (G-CSF) Monoclonal antibodies Tissue necrosis factor	EPO Thrombopoietin Insulin-like growth factor-1 Insulin hGH
30	<u>Cardiovascular Disease</u> Tissue Plasminogen Activator Streptokinase (native or chimeric)	
35	Urokinase (native or chimeric) α -antitrypsin antithrombin-III Other proteases or protease inhibitors	
40	Apolipoproteins (particularly B- 48) Circulating Scavenger Receptor APO A ₁	
	1 For treatment of severe combined immunodeficiency	
45	2 Converts low-density lipoproteins to high-density lipoproteins	

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As discussed above, chimeric proteins, PN-1 variants, and cysteine-PEGylated proteins may be delivered within the formulations and by the routes of administration discussed above. The particular
5 formulation, exact dosage, and route of administration will be determined by the attending physician and will vary according to each specific situation. Such determinations are made by considering such variables as the condition to be treated, the protein to be
10 administered, the pharmacokinetic profile of the particular protein, as well as various factors which may modify the effectiveness of the protein as a drug, such as disease state (e.g. severity) of the patient, age, weight, gender, diet, time of administration, drug
15 combination, reaction sensitivities, tolerance to therapy, and response to therapy. Long-acting protein drugs might only be administered every 3 to 4 days, every week or once every two weeks. Where cysteine-PEGylated proteins are used in the pharmaceutical composition, the
20 clearance rate (i.e. the half-life of the protein) can be varied to give ultimate flexibility to fit the particular need of the patient by changing, for example, the number of PEG moieties on the cysteine-protein, the size of the PEG moiety

25 Where cysteine-PEGylated proteins are employed, the daily regimen should generally be in the range of the dosage for the natural, recombinant, or PEGylated protein. Normal dosage amounts may vary from 0.1 to 100 micrograms, up to a total dose of about 1 g, depending
30 upon the route of administration. Guidance as to particular dosages for particular proteins is provided in the literature with respect to the administration of either native proteins and/or proteins PEGylated by conventional methodologies. For example, guidance for
35 administration of antithrombin-III for the prevention of

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fibrin clot formation may be found in USPNS 5,292,724 and 5,182,259; guidance for administration of human growth hormone (hGH) in the treatment of individuals intoxicated with poisonous substances may be found in USPNS 5,140,008
5 and 4,816,439; guidance for administration of hGH in the treatment of topical ulcers may be found in USPN 5,006,509; guidance for administration of (EPO) for treatment of anemia and pulmonary administration of EPO may be found in USPN 5,354,934; guidance for
10 administration of EPO, GM-CSF, G-CSF, and multi-CSF for treatment of pancytopenia may be found in USPN 5,198,417; guidance for administration of EPO for treating iron overload may be found in USPN 5,013,718; guidance for administration of EPO in the treatment of
15 hemoglobinopathies may be found in USPN 4,965,251; guidance for administration of insulin in the treatment of diabetes may be found in USPN 4,478,822; guidance for delivery of asparaginase for treatment of neoplasms may be found in USPNS 4,478,822 and 4,474,752; guidance for
20 administration of L-asparaginase in the treatment of tumors is found in USPN 5,290,773; guidance for administration of prostaglandin E1, prostaglandin E2, prostaglandin F2 alpha, prostaglandin I2, pepsin, pancreatin, rennin, papain, trypsin, pancrelipase,
25 chymopapain, bromelain, chymotrypsin, streptokinase, urokinase, tissue plasminogen activator, fibrinolysin, deoxyribonuclease, sultilains, collagenase, asparaginase, or heparin in a cryogel bandage for treatment of sites of trauma may be found in USPN 5,260,066; guidance for the
30 administration of superoxide dismutase, glucocerebrosidase, asparaginase, adenosine deaminase, interferons (alpha, beta, and gamma), interleukin (1,2,3,4,5,6,7), tissue necrosis factor (TNF-alpha or TNF-beta), and colony stimulating factors (CSF, G-CSF,
35 GM-CSF) in liposomes may be found in USPN 5,225,212;

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guidance for administration of asparaginase or insulin in the treatment of neoplastic lesions may be found in USPN 4,978,332; guidance for administration of asparaginase in the reduction of tumor growth may be found in USPN 4,863,910; guidance for the administration of antibodies in the prevention of transplant rejection may be found in USPNs 4,657,760 and 5,654,210; guidance for the administration of interleukin-1 as a therapy for immunomodulatory conditions including T cell mutagenesis, induction of cytotoxic T cells, augmentation of natural killer cell activity, induction of interferon-gamma, restoration or enhancement of cellular immunity, and augmentation of cell-mediated anti-tumor activity may be found in USPN 5,206,344; guidance for the administration of interleukin-2 in the treatment of tumors may be found in USPN 4,690,915; and guidance for administration of interleukin-3 in the stimulation of hematopoiesis, as a cancer chemotherapy, and in the treatment of immune disorders may be found in USPN 5,166,322.

All U.S. patents cited hereinabove are incorporated herein by reference with respect to the guidance provided in administration of the particular protein and/or PEGylated protein described therein.

Several PEGylated proteins have already been approved for use by the U.S. Food and Drug Administration (FDA). These PEGylated proteins include: hGH, insulin, interferon-alpha2A, interferon-alpha2B, tPA, EPO, G-CSF, and a hepatitis B vaccine which contains PEGylated proteins (Nucci et al. *ibid*).

Due to the usefulness of PEGylated proteins in therapy, there is a clear need for a method of generating PEGylated proteins at specific sites and which allows for the precise selection of amino acid residues for PEGylation, thus increasing the likelihood of generation

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of PEGylated proteins which retain the activity of the unmodified parent protein.

It is pointed out that PN-1 is not found in significant quantities in plasma and may function primarily in tissues. The high affinity heparin binding site of PN-1 appears to serve to localize PN-1 to connective tissues and cells which contain sulfated proteoglycans on their surface and surrounding extracellular matrix. Thus, the primary role of PN-1 seems to be in regulating proteolytic activity in tissues as opposed to blood. In that PN-1 is found in brain tissue another aspect of the invention involves delivering formulations of the invention containing PN-1 variants or chimeric proteins in order to facilitate peripheral or central nerve regeneration. Formulations, routes of administration and dosages for use of PN-1 in the treatment of inflammation and wounds are described in USPNs 5,206,017; 5,196,196; and 5,112,608; each of which are incorporated herein by reference to the extent that such methods of treatment using PN-1 are described.

It is generally not possible to obtain desirable results by administering large protein compounds such as chimeric proteins or protease nexin-1 and its variants by oral delivery systems. Such proteins are generally digested in the GI tract (unless formulated with special carriers) and do not enter the cardiovascular system in their original forms due to such digestion. Chimeric proteins, PN-1 variants, and/or cysteine-PEGylated versions of these proteins can be administered by any type of injection, such as intramuscular or intravenous, thus avoiding the GI tract. Other modes of administration include transdermal and transmucosal administrations provided by patches and/or topical cream compositions. Transmucosal administrations can include nasal spray formulations which include the chimeric

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proteins, protease nexin-1 variant, and/or cysteine-PEGylated proteins within a nasal formulation which contacts the nasal membranes and diffuses through those membranes directly into the cardiovascular system.

5 PEGylated proteins may have an increased ability to cross membranes and thus may enter the body more easily. Formulations which include the chimeric proteins, PN-1 variants within aerosols for intrapulmonary delivery are also contemplated by this invention, as are intraocular

10 delivery systems wherein the chimeric proteins or PN-1 variants are included within ophthalmic formulations for delivery in the form of eye drops.

Any of the above suggested means of administration could be provided in a variety of different formulations.

15 The formulations can be designed to provide the chimeric proteins or PN-1 variants systemically or to a particular site. Further, the formulations can be designed so as to provide the chimeric proteins or PN-1 variants as quickly as possible or in a sustained release or timed released

20 manner. For example, topical formulations could be created whereby the chimeric proteins or PN-1 variants of the invention were incorporated or disbursed throughout topical polymer formulations capable of slowly releasing the chimeric proteins or PN-1 variants to a wound site in

25 order to continually aid in wound healing and in preventing inflammation.

As indicated above, different formulations of the invention can be administered in a variety of different manners in order to introduce the chimeric proteins, PN-1

30 variants, and/or cysteine-PEGylated protein into the cardio vascular system. The chimeric proteins, PN-1 variants, and/or cysteine-PEGylated proteins are administered for a variety of purposes which generally relate to, for example: blocking proteolytic activity;

35 inhibition of tumor growth or metastasis; promotion of

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wound healing and/or nerve fiber regeneration;
replacement therapy for protein-deficient states (e.g.
diabetes); inhibition of bacterial, fungal, or viral
growth; enhancement of the immune response; induction of
5 maturation of bone marrow stem cells (e.g. in bone marrow
transfers); regulation of blood clotting; treatment of
inflammation; or treatment of bacterial sepsis and
endotoxic shock; replacement of albumin or hemoglobin
(e.g. to replace blood transfusions). In particular,
10 intravenous formulations containing the chimeric
proteins, PN-1 variants, and/or cysteine-PEGylated
versions of these proteins are useful for their
anti-thrombolytic effect and therefore can be
administered to aid and a prevention and/or alleviation
15 of strokes and/or heart attacks.

EXAMPLES

The following examples are provided so as to give
those of ordinary skill in the art a complete disclosure
and description of how to make and use the PN-1 variants
20 of the invention and are not intended to limit the scope
of what the inventors regard as their invention. Efforts
have been made to insure accuracy with respect to the
specifics given such as the association rate constants
and temperature but some experimental errors and
25 deviations should be accounted for. With respect to the
formulation examples, parts are parts by weight, and any
temperature readings are in degrees centigrade and all
experiments were carried out at or near atmospheric
pressure.

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EXAMPLE AThe Synthesis of PN-1

PN-1 was purified to homogeneity from serum-free medium conditioned by human foreskin fibroblasts in microcarrier cultures by affinity chromatography on heparin-agarose, followed by gel exclusion chromatography, as described in detail by Scott, R.W. et al., J Biol Chem (1985) 260:7029-7034, incorporated herein by reference. Of course, other chromatographic supports which contain heparin for affinity binding or other matrix such as cm sepharose or S-sepharose can also be used. The purified protein shows an M_r of 42-43 kd, based on sedimentation equilibrium analysis, or of 47 kd, estimated from gel-exclusion chromatography. The purified material shows the properties exhibited by PN-1 when contained in conditioned medium, including formation of sodium dodecylsulfate-stable complexes with thrombin, urokinase, and plasmin; inhibition of protease activity; heparin-enhanced inhibition of thrombin; and cellular binding of protease-PN complexes in a heparin-sensitive reaction. The N-terminal amino acid sequence of the isolated, purified protease nexin was determined for the first 34 amino acids to be: Ser-His-Phe-Asn-Pro-Leu-Ser-Leu-Glu-Glu-Leu-Gly-Ser-Asn-Thr-Gly-Ile-Gln-Val-Phe-Asn-Gln-Ile-Val-Lys-Ser-Arg-Pro-His-Asp-Asn-Ile-Val-Ile.

The PN-1 variants of the present invention can be synthesized by utilizing the pure PN-1 which has been isolated and purified in the manner indicated above. The variants can be obtained by cleaving the purified PN-1 protein at the P_1 or P_1' site and replacing the arginine, serine or both residues at that site with the desired non-polar substitute residue. After replacement of the desired residue with the desired non-polar residue, the segments can be fused utilizing protocols known to those skilled in the art. Although such methodology could be

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utilized in order to obtain the variants of the present invention, this methodology is somewhat cumbersome and is extremely limited, due to the very small amounts of PN-1 which can be extracted and purified. Accordingly, although the above procedure could be utilized, it is not the preferred method of making PN-1 or the variants disclosed herein. PN-1 and its variants are generally produced utilizing recombinant technology, as described below.

EXAMPLE B

A Generalized Recombinant Synthesis of PN-1

Methods of producing protease nexin-1 utilizing recombinant technology are disclosed within published European patent application 873049126 which published application is incorporated herein by reference to disclose recombinant technologies utilized in producing protease nexin-1. The procedure can be modified by those skilled in the art, reading this disclosure, to obtain PN-1 variants.

cDNA encoding the complete human PN-1 protein was obtained from a foreskin fibroblast DNA library. The retrieval of this clone took advantage of probes based on the amino acid sequence determined in the native protein. The cloned cDNA is amenable to expression in recombinant cells of both procaryotic and eucaryotic organisms by excising the coding sequence from the carrier vector and ligating it into suitable expression systems.

The PN-1 can be directly produced as a mature protein preceded by a Met N-terminal amino acid (which may or may not be processed, depending on the choice of expression systems) may be produced as a fusion protein to any desirable additional N-terminal or C-terminal sequence, or may be secreted as a mature protein when preceded by a signal sequence, either its own, or a

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heterologous sequence provided by, for example, the known signal sequence associated with the bacterial-lactamase gene or with secreted human genes such as insulin or growth hormones. Means for providing suitable
5 restriction sites at appropriate locations with respect to the desired coding sequence by site-directed mutagenesis are well understood, and the coding sequence can thus be provided with suitable sites for attachment to signal sequence or fusion sequence, or into expression
10 vectors.

If bacterial hosts are chosen, it is likely that the protein will be produced in nonglycosylated form. If the PN-1 is produced intracellularly as a "mature" protein, the N-terminal methionine may be only partially
15 processed, or not processed at all. Thus, the protein produced may include the N-terminal Met. Modification of the protein produced either intracellularly or as secreted from such bacterial host can be done by providing the polysaccharide substances, by refolding
20 using techniques to sever and reform disulfide bonds, or other post-translational ex vivo processing techniques. If the protein is produced in mammalian or other eucaryotic hosts, the cellular environment is such that post-translational processing can occur in vivo, and a
25 glycosylated form of the protein is most likely produced.

The recombinant cells are cultured under conditions suitable for the host in question, and the protein is recovered from the cellular lysate or from the medium, as determined by mode of expression.
30 Purification of the protein can be achieved using methods similar to that disclosed by Scott, R.W. et al., J Biol Chem (supra), or by other means known in the art.

Once DNA segments coding for the production of PN-1 have been inserted into bacterial hosts, multiple
35 copies of the segments can, of course, be cloned by

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growing the bacteria. The segments can be extracted from the bacteria by the use of conventional methodology whereby the DNA is extracted by subjecting disrupted cells to centrifugation and then subjecting the extracted DNA to enzyme digestion, which will result in obtaining the desired segments by subjecting the digested DNA to separation processes such as gel electrophoresis and blotting. The segments coding for the production of PN-1 can then be subjected to conventional recombinant methodologies in order to substitute codons coding for the arginine and/or serine with new codons which code for the production of the desired non-polar amino acid residue. Once such recombinant segments are produced, they can be reinserted into vectors and hosts in the manner described above in order to obtain the production of the desired PN-1 variants. A variety of vector and host systems known to those skilled in the art can be used.

In addition, it is pointed out that PN-1 variants might be made by using recombinantly produced PN-1 and then substituting only the desired "R" group (e.g., -OH of serine 346) with a non-polar "R" group (e.g., -CH₂CH₂-S-CH₃) to get a PN-Met₃₄₆ variant. Such replacements of the "R" group can be carried out using published protocols known to those skilled in the art.

EXAMPLE C

Production of Recombinant PN-1 Variants in Insect Cells Using a Baculovirus Expression System

C.1. Construction of plasmid expression vector:

In order to produce PN-1 and/or PN-1 variants in insect cells, the cDNA sequence must first be inserted into a suitable plasmid expression vector, such as pAC373. Appropriate restriction sites for this insertion

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can be created by standard site-directed mutagenesis procedures. The essential properties of a suitable expression vector include a transcriptional promoter such as the polyhedron gene promoter of pAC373, and flanking
5 homologous sequences to direct recombination into the baculovirus genome. A polyadenylation signal, such as the one from the polyhedron gene present in this plasmid vector, may or may not be necessary for expression of the recombinant gene. A marker gene such as the β -
10 galactosidase gene of E. coli, juxtaposed to regulatory sequences including a transcriptional promoter and possibly a polyadenylation signal, may be included in the vector but is not essential for expression of a convected gene.

15 C.2. Creation of recombinant baculovirus:

A chimeric baculovirus is created by homologous recombination between the expression plasmid containing the PN-1 target gene and wild type baculovirus DNA. Plasmid and wild type baculovirus DNA are co-precipitated
20 by the calcium phosphate technique and added to uninfected Spodoptera frugiperda (Sf9) insect cells. Four to seven days following transfection, cells will exhibit a cytopathic morphology and contain the nuclear occlusion bodies typically produced by viral infection.
25 The cell-free culture media containing both wild type and recombinant virus is harvested.

C.3. Identification and isolation of chimeric baculovirus:

Clonal isolates of virus can be obtained from this
30 co-transfection stock by plaque purification on Sf9 cell monolayers overlaid with agarose. Candidate plaques for analysis will be identified by a plaque morphology negative for occlusion bodies. If the expression plasmid

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contains a marker gene such as β -galactosidase, recombinant plaques will be indicated by the blue color produced from a chromogenic substrate such as 5-bromo-4-chloro-3-indolyl- β -D-galactopyranoside (X-gal) in the agarose plating medium. Picked plaques will be used for inoculation of cells in multiwell dishes. The resulting cell lysates and infected cell supernatants can be evaluated for expression of recombinant PN-1, using standard activity or immunological assays. Positive wells may require additional rounds of plaque purification to obtain pure recombinant virus stocks free from wild type contamination.

C.4. Batch production of PN-1:

Sf9 cells are adapted to growth in serum-free, low protein medium such as ExCell (J.R. Scientific). Cells are collected from suspension culture by gentle centrifugation and resuspended in fresh medium containing the viral inoculum at a concentration of ten million cells per ml., using a multiplicity of infection of one virus plaque forming unit per cell. After a period of two hours, the culture is diluted five fold with fresh medium and incubated two to three days. At the end of that time, the cells are pelleted by centrifugation and the conditioned medium harvested. PN-1 is purified from the cell-free supernatant by standard means.

Variants of PN-1 may be created and produced in the same manner as described above.

C.5. Characterization of insect cell derived PN-1:

PN-1 produced in insect cells using a baculovirus expression system is a glycosylated protein of approximate molecular weight of 42,000 kd. The N-terminal amino acid sequence is identical to that of

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mature mammalian cell PN-1, indicating correct processing of the signal sequence. The specific activity vs thrombin and association kinetics, including rate enhancement effect of heparin, are indistinguishable from authentic PN-1.

EXAMPLE D

Production of Recombinant PN-1 Variants in E. coli in Inclusion Bodies or in Soluble Form

D.1 Cloning of PN-1

10 The cloning of PN-1 and expression has been described (McGrogan, et al., (1988) Bio/Technology). The gene for PN-1 was generated by PCR from the CHO expression vector using the following oligonucleotides: PNPCR-forward 5' TG.GAA.GGA.CAT.ATG.AAC.TGG.CAT.CTC
15 PNPCR-reverse 5' TCT.TTT.GTA.TAC.TGA.TCA.GGG.TTT.GT generating an NdeI and BclI site, respectively. The resulting fragment was cut with NdeI and BclI and subcloned into pGEMEX-1 vector (Promega).

 The pGEMEX E. coli expression vector contains
20 three RNA polymerase promoters. The T7 promoter is positioned upstream from the gene 10 leader fragment.

 We removed the gene 10 region from pGEMEX, but retained the T7 RNA polymerase binding site and NdeI and BamHI cloning sites. To accomplish this the NdeI site at
25 3251 in pGEMEX was removed by partial NdeI digest followed by Klenow fill-in and relegation. This plasmid is referred to as pT7-NK. pT7-NK was cut with NdeI and BamHI to remove the gene 10 fusion protein region. The linear vector was isolated and ligated with the PCR-
30 generated PN-1 linear fragment, cut with NdeI and BclI, described above. This plasmid is referred to as pT7PN-1. The correct sequence was confirmed by sequencing the entire coding region for PN-1.

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The native signal sequence was removed using PCR and the following oligos:

PCRMET.forward 5'GAT.ATA.CAT.ATG.TCC.CAC.TTC.AAT.CCT.CTG

PCRMET.reverse 5'GGG.GGC.ACT.TGT.CGA.CCC.ACA.CCG.GAA

5 with an NdeI and SalI site, respectively. This generated a 690 base pair fragment which could replace the native signal and a portion of the amino terminus of PN-1 with a start codon (Met) and the amino terminus of PN-1. Again, the correct sequence was confirmed by sequencing. The
10 expression of the resulting protein is expected to be intracellular, either in inclusion bodies or as soluble protein.

D.2. Mutagenesis of PN-1

The plasmid pT7PN1 has an f1 ori for the
15 production of single-stranded DNA. Thus pT7PN1 was transformed into the E. coli strain CJ236 for the production of ssDNA to be used as a template for site-directed mutagenesis according to the method of Kunkel (Kunkel, T.A. (1988) in Nucleic Acids and Molecular
20 Biology (Eckstein, F., Lilley, D.M.J. Eds.) Vol. 2, p. 124, Springer-Verlag, Berlin and Heidelberg).

The general rationale for mutant generation is based upon four general methods.

In the first method, single amino acid
25 substitutions in the region of P4 to P4' are generated by site directed mutagenesis. In general, substitutions at the P1 site will have the most dramatic effects. However, substitutions at other residues within the active site region will give changes in association rate
30 constants with serine proteases.

In the second method, sequences found at the active site region of other serpins were grafted onto PN-1. A number of combinations must be created to determine how much of the sequence at the active site

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must be changed to change the specificity and kinetics. The P₄ to P₄' region is generally found to be most important, but amino acids residues outside this region can have pronounced affects on protease inhibition.

5 In the third method, sequences which have been found to be particularly good substrates are added to or used to replace a sequence of PN-1. Prior to making these mutants, it was not clear if these changes would ruin the inhibitory effects of PN-1 and turn PN-1 from an
10 inhibitor of proteolysis into a substrate. In fact, incorporation of Ala-Ala-Pro-Phe, a good substrate sequence for subtilisin, into PN-1 results in a molecule which is cleaved particularly well by subtilisin. However, PN-1 variants have now been obtained which are
15 good inhibitors of mammalian serine proteases based upon this approach.

 In the fourth method, optimum inhibitor sequences can be generated by using a phage display system. Since PN-1 forms covalent interactions with the target
20 protease, it is important that one is not selecting for mutants which bind more tightly than the parent PN-1 molecule. Rather, one selects for PN-1 variants which bind more rapidly to the target protease by allowing phage-displayed variant PN-1 library to interact with the
25 immobilized target protease for only short times. Thus, only rapid-binding variants will be selected. This is a novel application of the phage display system.

 The following oligonucleotides were used to generate a mutant specific for the protease shown at the
30 end of the sequence:

5'GCA.ATT.CTC.ATT.GCA.NN(G/C).TCA.TCG.CCT.CCC [R345I, R345M, R345L, R345V] (elastase), R345K (plasmin), R345D, R345E 5'ATT.CTC.ATT.GCA.GTG.AGC.TCG.CCT.CCC.TG R345V (elastase)

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- 5'ATT.CTC.ATT.GCA.AGA.ATA.TCG.CCT.CCC.TGG S3461
(Factor Xa)
5'ATT.CTC.ATT.GCA.AGA.ACA.TCG.CCT.CCC.TCC S346T
(Factor Xa, C1-esterase)
- 5 5'ACA.ACT.GCA.ATT.CTG.GCT.GGA.AGA.TCA.TTG.AAT.CCC.TGG.
TTT.ATA I343A;A344G;S347L;P348N (ATIII-like, thrombin,
Factor Xa)
5'ACA.ACT.GCA.ATT.CTC.TTT.CCA.AGA.TCA.TCG.CCT.CCC
I343F;A344P (FPR, thrombin)
- 10 5'ACT.GCA.ATT.CTC.ATT.CCA.TTA.TCA.TCG.CAG.GTC.CGG.TTT.
ATA.GTA.GAC A344P;R345L;P348Q;P349V;W350R (HCII-
like)
5'GAA.GAT.GGA.ACC.AAA.GCT.TCA.GAC.TTT.TTG.GCT.GAA.GGT.
GGC.GGT.GTA.AGA.TCA.TCG.CCT.CCC.TGG A336D;A337F;
15 T338L;T339A;A340E;I341G;L342G;A344V (fibrinogen-
like, thrombin)
5'GCA.ACA.ACT.GCA.ATT.ATC.GAG.GGA.AGA.TCA.TCG.CCT
L342I;I343E;A344G (Factor Xa)
- 20 5'ACA.ACT.GCA.ATT.CTC.GAG.CCA.GTA.TCA.TCG.CCT.CCC
I343E;A344P;R345V (elastase, cathepsin G)
5'ACT.GCA.ATT.CTC.ATT.GGA.AGA.TCA.TCG.CCT A344G (faster
kinetics)
5'ACT.GCA.ATT.CTC.ATT.CCA.AGA.TCA.TCG.CCT A344P (faster
kinetics)
- 25 5'GCA.ACA.ACT.GCA.ATT.AGC.CCT.TTC.AGA.TCA.GTG.CAG.CCC
TGG.TTT.ATA L342S;I343P;A344F;S347V;P348Q (high
molecular weight kininogen-like; kallikrein)
5'GCA.ACA.ACT.GCA.ATT.GCC.GCT.CCA.TTC.TCA.TTG.CCT.CCC.
TGG.TTT L342A;I343A;A344P;R345F (cathepsin G)
- 30 5'GCA.ACA.ACT.GCA.ATT.GCC.GCT.CCA.GTA.TCA.TCG.CCT.CCC.
TGG.TTT L342A;I343A;A344P;R345L (elastase)
- 5'GCA.ACA.ACT.GCA.ATT.GCC.GCT.CCA.CTA.TCA.TCG.CCT.CCC.
TGG.TTT L342A;I343A;A344P;R345L (elastase)
5'GCA.ACA.ACT.GCA.ATT.GCC.GCT.CCA.ATA.TCA.TCG.CCT.CCC.

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TGG.TTT L342A;I343A;A344P;R345I (elastase)

D.3. Expression and Purification of Protease Nexin
Variants in E. coli

JM109 (DE3) contains a chromosomal copy of the
5 gene which codes for T7RNA polymerase under the control
of the inducible lac promoter. JM109 (DE3) containing
pT7PN-1 (or a variant of PN-1) was grown overnight in
2xYT + 0.2% glucose + 100 mg/ml carbenicillin at 28-32°C.
Low temperature and high nutrient containing solution is
10 helpful in generating productive inoculants. The
inoculum was diluted 1:250 to 1:500 and grown to OD₆₀₀~1
in a shake flask or ~50 in a fermentor at 26-37°C, and
induced with IPTG at 0.1-1.0 mM for 4-16 hours. The
bacteria were collected by centrifugation, resuspended in
15 10 mM TRIS, pH 8, 1 mM EDTA, and disrupted by high
pressure homogenization. Inclusion bodies were collected
by centrifugation, washed with 1 M NaCl, 0.05%
triethylamine, and the protein refolded from a 6 M
guanidine solution by rapid dilution. PN-1 was purified
20 by capture on FastS sepharose and eluted with 0.6 M NaCl,
diluted to 0.25 M NaCl and passed over FastQ sepharose to
remove endotoxin and recaptured on FastS sepharose and
eluted with 0.6 M NaCl or a gradient of 0.25 to 1 M NaCl.

Alternatively, PN-1 can be generated in a soluble
25 form within E. coli by adjusting the fermentation
conditions. This procedure provides a greater yield of
soluble PN-1 as the fermentation temperature is decreased
from 37°C to 26°C with a concomitant loss in inclusion
body material. This is quite an unexpected finding,
30 since PN-1 is bactericidal when native PN-1 is added to
E. coli. To purify soluble PN-1, the cell supernatant
from the disruption step was clarified by centrifugation
and filtration or by treatment with polycations such as
polyethyleneimine or Biacryl™ followed by centrifugation

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and filtration, and the soluble protein was purified as above. The generation of soluble material has many advantages: there is more certainty that the protein is correctly folded, there are no refolding steps, there is
5 greater reproducibility from batch to batch.

The production of PN-1 was about 50 mg per gram of cell paste. This corresponds to about 50 mg per liter of production at a cell density of 1 OD₆₀₀ or up to 2.5 grams of soluble PN-1 per liter of fermentation.
10 This represents a substantial advance in the state of the art of PN-1 production.

D.4. Activity assay for PN-1 Variants

Refolded or soluble protein was tested for capacity to inhibit thrombin in a standard assay.
15 Briefly, serial 2-fold dilutions of PN-1 variant were added to microtiter plate wells (50 μ l/well), followed by 50 μ l of a 30 μ g/ml heparin solution, followed by 1 NIH unit of thrombin in 50 μ l. These were allowed to incubate at 25°C for 15 minutes. Residual thrombin
20 activity was measured by the addition of 50 μ l S-2238 (Kabi Pharmaceuticals) at 0.625 mg/ml. PN-1 variants were tested for their ability to inhibit urokinase using the substrate S-2444, plasmin using the substrate S-2390, tPA using the substrate S2288, Factor Xa using the
25 substrate S-2222 or S-2765, kallikrein using the substrate S-2302, human neutrophil elastase using s-AAPV-pna (Sigma), cathepsin G using s-AAPF-pna (Sigma) in a similar manner, with or without the addition of heparin.

30 The second-order rate association constants were determined for appropriate inhibitors-proteases combinations by combining equal-molar amounts of each protein (determined by titration as above) for various times from 1 second to 4 hours (as appropriate) and

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following the activity loss. The $t_{1/2}$ was estimated from resulting curves. The k_{assoc} was estimated according to the equation $\ln 2 / [PN-1] \times t_{1/2}$. Alternatively, the apparent first order rate constant was determined from the slope of a plot of log (normalized activity) vs time. The second order rate constant was calculated by dividing the apparent first order rate constant by the PN-1 (or variant) concentration used.

EXAMPLE E

10 Generation of ATF-PN1 Chimera

To generate this chimera, we first cloned the amino-terminal fragment of uPA by PCR using the oligonucleotides: ATF.forward

5'GGT.GAT.CAT.ATG.AGC.AAT.GAA.CTT.CAT.CAA

15 ATF.REVERSE

5'TTT.AGG.ACG.CGT.CTG.CGC.CAT.CTG.CTC.AGT.CAT.G

generating a NdeI and MluI site respectively. The resulting fragment was cut with NdeI and MluI and subcloned into pT7PN1 vector cut with the same enzymes to move the signal sequence. This plasmid is referred to as pT7ATF-PN1. The correct sequence was verified by automated sequencing using the T7 dye primer system (ABI).

To generate an even shorter version of ATF-PN1 which retains the urokinase receptor binding region, ATF₄₈-PN1 was made by introducing a MluI site (underlined) by site directed mutagenesis at codon 48 using the following oligonucleotide:

5'CAC.TGT.GAA.ATA.GAT.AAC.GCG.TAA.ACC.TGC.TAT.GAG.

30 The resulting plasmid was cut with MluI to remove a 300 bp segment and ligated.

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Mutagenesis of ATF-PN1

The plasmid pT7ATF-PN1 has an f1 ori for the production of single-stranded DNA. Thus pT7ATF-PN1 was transformed into the E. coli strain CJ236 for the production of ssDNA to be used as a template for site-directed mutagenesis according to the method of Kunkel (Kunkel, T.A. (1988) in *Nucleic Acids and Molecular Biology* (Eckstein, F., Lilley, D.M.J. Eds.) Vol. 2, p. 124, Springer-Verlag, Berlin and Heidelberg). In addition, PN-1 variants of interest can be subcloned into pT7ATF-PN-1 by using standard molecular biology techniques.

Expression and Purification of ATF-PN1

The resultant plasmid was transformed into the E. coli strain JM109 (DE3), grown to OD₆₀₀ ~1 in a shake flask or ~50 in a fermentor, and induced with IPTG at 0.1-1.0 mM for 4-16 hours at 26-37°C. The bacteria were collected by centrifugation, resuspended in 10 mM TRIS, pH 8, 1 mM EDTA, and disrupted by high pressure homogenization. Inclusion bodies were collected by centrifugation, washed with 1 M NaCl, 0.05 % TEA, and the protein refolded from a 6 M guanidine solution. ATF-PN1 was purified by capture on FastS sepharose and eluted with 0.6 M NaCl, diluted to 0.25 M NaCl and passed over FastQ sepharose to remove endotoxin and recaptured on FastS sepharose and eluted with 0.6 M NaCl or a gradient of 0.25 to 1 M NaCl. Alternatively, the cell supernatant from the disruption step was clarified by centrifugation and filtration, and the soluble protein was purified as above.

Activity assay for ATF-PN1

Refolded or soluble protein was tested for capacity to inhibit thrombin in a standard assay.

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Briefly, serial 2-fold dilutions of ATF-PN1 were added to microtiter plate wells (50 μ l/well), followed by 50 μ l of a 30 μ g/ml heparin solution, followed by 1 NIH unit of thrombin in 50 μ l. These are allowed to incubate at 25°C for 15 minutes. Residual thrombin activity is measured by the addition of 50 μ l S-2238 (kabi Pharmaceuticals) at 0.625 mg/ml. ATF-PN1 was tested for its ability to inhibit urokinase using the substrate S-2444, or plasmin using the substrate S-2390, in a similar manner, without the addition of heparin.

Refolded or soluble protein was tested for the ability to bind to a soluble form of the urokinase receptor as measured by ELIZA, or the ability to inhibit the binding of urokinase to the soluble urokinase receptor. ATF-PN1 was also tested for its ability to inhibit uPA or DFP/PMFS treated uPA binding to cells such as HT1080, U937, or THP-1 expressing uPA receptor.

EXAMPLE F

Generation of Cysteine-PEGylated Proteins

20 F.1 Preparation of Maleimido-PEG Reagent

Maleimido-PEG was prepared by mixing the following:

- 1) 100 mg methoxypolyethylene amine (20 μ mol) (MW \approx 5,000)
- 25 2) 20 μ mol γ -maleimidobutyric acid-N-hydroxy succinimide ester (GMBS)
- 3) 2 ml 100 mM Caps buffer, pH 10.0

The amount of the components above (particularly 1) and 2)) and the volume indicated may be varied. For example, it is permissible that the difference in the ratio of methoxypolyethylene amine to GMBS can vary by up to ten to 100-fold. Normally, about a two-fold excess of 1)

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above to GMBS is preferred. While various buffers may be substituted for the Caps buffer, it is important that Tris buffers are not used in this mixture, as Tris buffers will quench the reaction. The pH of the buffer used may vary considerably, although buffers having a pH of 10.0 are preferable over buffers having a pH of 8.0. In addition, the mixture above may contain up to 50% DMSO as a cosolvent. It is particularly important that the reaction mixture does not contain a reducing agent such as dithiothreitol (DTT) or β -mercaptoethanol (β ME).

The mixture was incubated at 37°C for 30 minutes, although the reaction temperature may be as low as 4°C and the reaction time may be extended for up to one hour or more. After incubation, 12 mg of Tris free base or ethanolamine was added to the mixture to quench the NH_3 moiety. This quenching step may be omitted.

The reacted mixture is purified by elution through a PD-10 column (G-25) (BioRad) equilibrated with 20 mM Tris (pH 7.4), 100 mM NaCl, and 0.1% Tween. The eluant was collected in 0.5 ml fractions and assayed for production of the Maleimido-PEG reagent by precipitation with 50% TCA. The resulting Maleimido-PEG (Mal-PEG) reagent is then used in to modify a selected protein by attachment of PEG to a cysteine residue(s).

25 F.2 Reaction of Maleimido-PEG with Protein

Prior to reaction of the protein with the Maleimido PEG reagent, the purified protein was diluted to a concentration of about 200 $\mu\text{g/ml}$ to 1 mg/ml in any suitable buffer which does not contain DTT or β ME. Normally, the buffer was composed of 20 mM PIPES pH 6.75, 0.6 M NaCl, and 1% glycerol. Approximately 10 μl to 40 μl of the diluted protein was used for the PEGylation reaction. The Maleimido-PEG reagent described in section F.1 was diluted in a series of 2-fold dilutions using

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10 μ l transfers of solution containing approximately 1
10 μ l Maleimido-PEG in a 10 μ l volume of buffer composed of
20 mM Tris pH 7.4, 0.1 M NaCl, and 0.01% Tween. The
ratio of the maleimido-PEG to protein may be varied
5 according to the preferred level of PEGylation of the
protein desired. Up to 20-fold excess of maleimido-PEG
to protein still provided for specific reaction of the
reagent with cysteine residues of the protein.

The protein and maleimido-PEG were incubated for
10 one hour at room temperature, although this reaction may
be performed at 4°C for longer periods of time. A sample
of the reacted mixture may be analyzed by SDS-PAGE to
determine the minimal amount of maleimido-PEG reagent
needed for complete coupling.

15 The reaction described above may be used to
determine the proper ratio of Maleimido-PEG to protein,
and then scaled up to produce commercially acceptable
amounts of PEGylated protein.

F.3 Preparation of (Maleimido)₂-PEG Reagent

20 (Maleimido)₂-PEG is prepared by mixing the
following:

- 1) polyethylene bis[amine]
- 2) 20 μ mol γ -maleimidobutyric acid-N-hydroxy
succinimide ester (GMBS)
- 25 3) 2 ml 100 mM Caps buffer, pH 10.0

The amount of the components above (particularly 1) and
2)) and the volume indicated may be varied. For example,
it is permissible that the difference in the ratio of 10
and 2) can vary by up to 10 to 100 fold, although an
30 excess of GMBS to 1) above is preferred, normally about a
2-fold excess. While various buffers may be substituted
for the Caps buffer, it is important that Tris buffers
are not used in this mixture, as Tris buffers will quench

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the reaction. The pH of the buffer used may vary considerably, although buffers having a pH of 10.0 are preferable over buffers having a pH of 8.0. In addition, the mixture above may contain up to 50% DMSO as a
5 cosolvent. It is particularly important that the reaction mixture does not contain a reducing agent such as dithiothreitol (DTT) or β -mercaptoethanol (β ME).

The mixture is incubated at 37°C for 30 minutes, although the reaction temperature may be as low as 4°C
10 and the reaction time may be extended for up to one hour or more. After incubation, 12 mg of Tris free base or ethanolamine is added to the mixture to quench the NH_2 moiety. This quenching step may be omitted.

The reacted mixture is purified by elution through
15 a PD-10 column (G-25) (BioRad) equilibrated with 20 mM Tris (pH 7.4), 100 mM NaCl, and 0.1% Tween. The eluant is collected in 0.5 ml fractions and production of (Maleimido)₂-PEG is assayed by precipitation with 50% TCA. The resulting (Maleimido)₂-PEG (Mal-PEG) reagent is then
20 used in to modify a selected protein by attachment of PEG to a cysteine residue(s).

F.4 Reaction of (Maleimido)₂-PEG with Protein

Prior to reaction of the protein with the (Maleimido)₂-PEG reagent, the purified protein (e.g. a
25 PN-1 mutant containing a cysteine residue at position 99) is diluted to a concentration of about 200 $\mu\text{g/ml}$ to 1 mg/ml in any suitable buffer which does not contain DTT or β ME. Normally, the buffer is composed of 20 mM PIPES pH 6.75, 0.6 M NaCl, and 1% glycerol. Approximately
30 10 μl to 40 μl of the diluted protein is used for the PEGylation reaction. The (Maleimido)₂-PEG reagent described in section F.1 is diluted in a series of 2-fold dilutions using 10 μl transfers of solution containing approximately 1 μl (Maleimido)₂-PEG in a 10 μl volume of

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buffer composed of 20 mM Tris pH 7.4, 0.1 M NaCl, and 0.01% Tween. The ratio of the maleimido-PEG to protein may be varied according to the preferred level of PEGylation of the protein desired.

5 The protein and (Maleimido)₂-PEG are incubated for one hour at room temperature, although this reaction may be performed at 4°C for longer periods of time. A sample of the reacted mixture may be analyzed by SDS-PAGE to determine the minimal amount of (Maleimido)₂-PEG reagent
10 needed for complete coupling.

 The reaction described above may be used to determine the proper ratio of (Maleimido)₂-PEG to protein, and then scaled up to produce commercially acceptable amounts of PEGylated dimeric or multimeric proteins.
15

EXAMPLE G

Generation of Cysteine-PEGylated PN-1 Variants (Type IV Variants)

G.1 Selection of amino acid residues of PN-1 for 20 substitution by cysteine

 PN-1 α and PN-1 β contain N-glycosylation sites at amino acid residue positions 99 and 140. Therefore, these sites were selected for site-directed mutagenesis to replace the asparagine at one or both of these
25 positions with cysteine.

 Three sites in PN-1 were selected for replacement with cysteine on the basis of the presence of glycosylated residues at a corresponding site in a protein homologous to PN-1. Amino acid residue D192 was
30 selected for replacement with cysteine since the proteins angiotensin and Rab ORF1, each which are homologous to PN-1, are N-glycosylated at the amino acids corresponding to this residue in PN-1. Amino acid residue E230 was selected for replacement with cysteine since baboon α_1 -
35 antitrypsin (α_1 -AT), which is homologous to PN-1, is

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glycosylated at the amino acid residue corresponding to this position in PN-1. Amino acid residue H252 was selected for replacement with cysteine since α_2 -antiplasmin (α_2 -AP), another protein homologous to PN-1, is glycosylated at the corresponding residue.

Other amino acid residues were selected for replacement with cysteine on the basis of the position of the amino acid within the three-dimensional structure of PN-1 as determined by X-ray crystallography (Figure 3).

10 The approximate position of the amino acid residues selected for cysteine substitution are indicated by their corresponding amino acid residue number. The particular amino acid residues identified for mutagenesis in the present example were selected on the basis of the

15 apparent solvent-accessibility of the amino acid and the apparently few number of interactions with other amino acids in the protein.

G.2 Site-directed Mutation of PN-1 to Cysteine

The mutations selected above were generated in PN-1 α using site-directed mutagenesis as described in section D.2. Although PN-1 α was employed in these experiments, the same mutations in PN-1 β are likely to provide the same effects as all the mutations were introduced into the region of amino acid sequence

25 identity between these nearly identical proteins. Briefly, DNA encoding PN-1 was inserted into the plasmid pT7PN1, which has an f1 ori for the production of single-stranded DNA. This plasmid was then transformed into the E. coli strain CJ236 for the production of ssDNA to be used as a

30 template for site-directed mutagenesis according to the method of Kunkel (Kunkel, T.A. (1988) in Nucleic Acids and Molecular Biology (Eckstein, F., Lilley, D.M.J. Eds.) Vol. 2, p. 124, Springer-Verlag, Berlin and Heidelberg).

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The oligonucleotides used to generate specific mutations within the PN-1 coding region are as follows:

- 5 **N140C** AAT GCA TGG GTT AAA AAC GAA ACC AGG GAT
AAT GCA TGG GTT AAC TGC GAA ACC AGG GAT
HpaI
- N99C** GCC GTG TTT GTT AAG AAT GCC TCT GAA ATT
GCC GTG TTT GTT AAC TGT GCC TCT GAA ATT
HpaI
- 10 **P28C** GTG AAG TCG AGG CCT CAT GAC AAC ATC GTG ATC
GTG AAG TCG AGG TGC CAT GAC AAC ATC GTG ATC
- G52C** CTG GGG GCG GAC TGC AGG ACC AAG AAG
PstI
- 15 **N85C** GTC TCC AAG AAG AAT AAA GAC ATT GTG ACA GTG GCT
GTC TCC AAG AAG TGC AAA GAT ATC GTG ACA GTG GCT
EcoRV
- Q116C** AAA GAT GTG TTC CAG TGT GAG GTC CGG
AAA GAT GTG TTC TGC AGT GAG GTC CGG
PstI
- 20 **N304C** TCA TCA AAG GCA AAT TTT GCA AAA ATA ACA
TCA TCA AAG GCA TGC TTT GCA AAA ATA ACA
SphI
- S1C** GAT ATA CAT ATG TCC CAC TTC AAT CCT CTG TCT CTC GAG
GAT ATA CAT ATG TGC CAC TTC AAT CCC TTA AGT CTC GAG
AflIII
- 25 GAA CTA GGC
GAA CTA GGC
- R63C** AAG AAG CAG CTC GCC ATG GTG ATG AGA TAC GGC GTA AAT
AAG AAG CAG CTC GCA ATG GTG ATG TGC TAC GGC GTA AAT
NcoI destroyed
- 30 **E125C** GTC CGG AAT GTG AAC TTT GAG GAT CCA GCC TCT
GTC CGG AAT GTT AAC TTT TGC GAT CCA GCC TCT
HpaI
- D147C** AGG GAT ATG ATT GAC AAT CTG CTG TCC CCA GAT CTT ATT
AGG GAT ATG ATT TGC AAT CTC TTA AGC CCA GAT CTT ATT
AflIII
- 35

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5 E230C CCC TAC CAC GGG GAA AGC ATC AGC ATG
CCC TAC CAC GGC TGC AGC ATC AGC ATG
PstI

10 S263C ACC ATA GAC AGC TGG ATG AGC ATG GTC
ACC ATA GAC AGT TGG ATG TGC ATC ATG GTC
PvuII destroyed

P267C AGC ATC ATG GTC CCC AAG AGG GTG CAG
AGC ATC ATG GTC TGC AAA CGC GTG CAG
Afl III

D284C GCT GTA GCA CAA ACA GAT TTG AAG GAG CCG CTG
GCT GTA GCA CAA ACA TGT TTA AAG GAG CCG CTG
DraI

The mutants are named according to the single-letter code for the amino acid residue in the native protein, the number of the position of that amino acid within the amino acid sequence of PN-1, and the single-letter code for the amino acid residue substituted at that site. For example, the mutant S1C produces a PN-1 protein which has the serine at position 1 replaced by cysteine. The top sequence for each mutant above indicates the wild type PN-1 sequence, while the sequence below indicates the mutation introduced in the coding sequence of the mutant. The nucleotides in bold are changed relative to wild type. The codon which is double-underlined is the newly-introduced codon for cysteine. The underlined sequences in the mutated DNA sequence indicate a restriction enzyme site which is introduced into or removed from the nucleotide sequence of the mutant. Introduction or removal of these restriction sites do not alter the amino

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acid sequence encoded at that site, but provide a means for screening clones containing DNA subjected to site-directed mutagenesis for incorporation of the oligonucleotide sequence into the PN-1 coding sequence.

- 5 Introduction of the desired mutation was confirmed by restriction enzyme analysis.

- Mutant PN-1 proteins containing multiple cysteine-substituted residues were generated by introduction of a first mutation by site-directed mutagenesis as described.
- 10 After confirmation of the insertion of the first mutation by restriction enzyme analysis, the DNA was subjected to a second round of site-directed mutagenesis using a different oligonucleotide. For example, the double mutant N99C;N140C was generated by site-directed
- 15 mutagenesis with the N99C oligonucleotide and confirmation of the presence of the newly introduced HpaI site in the coding sequence. The N99C mutant DNA was then subjected to a second round of site-directed mutagenesis with the N140C oligonucleotide. Table G.5A
- 20 below lists the single, double, and triple mutants generated using these techniques and the oligonucleotides described above.

- DNA encoding the mutant PN-1 proteins were expressed and the expressed proteins purified as
- 25 described in section D.3.

G.3 Reaction of PN-1 and PN-1 Mutants with Maleimido-PEG Reagent

- After purification of PN-1 and the PN-1 mutants described above, each protein was reacted with the
- 30 Maleimido-PEG reagent described in F.1 according to the general protocol of F.2. For example, the mutant N99C;N140C was cysteine-PEGylated using the following protocol.

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Purified N99C;N140C protein was diluted to a concentration of about 200 µg/ml in 20 mM PIPES pH 6.75, 0.6 M NaCl, 1% glycerol. Approximately 40 µl of the diluted protein (0.25 nmol) was used for the PEGylation reaction. The Maleimido-PEG reagent described in section F.1 was diluted in a series of 2-fold dilutions using 10 µl transfers starting from approximately 2 µl Maleimido-PEG in a 10 µl volume of buffer composed of 20 mM Tris pH 7.4, 0.1 M NaCl, and 0.01% Tween. This reaction contained a two-fold excess of the Maleimido-PEG reagent over that required for PEGylation of the number of cysteine sites in the PN-1.

The N99C;N140C protein and maleimido-PEG mixtures were incubated for one hour at room temperature. A sample of each of the reacted mixtures was analyzed by SDS-PAGE. Analysis of this gel revealed that the band migrating at the relative molecular weight of unmodified N99C;N140C PN-1 disappeared as the ratio of Maleimido-PEG to protein increased. Accordingly, as the amount of unmodified N99C;N140C PN-1 in the sample disappeared with increasing Maleimido-PEG concentrations, distinct bands migrating at molecular weights of increasing intervals of approximately 5,000 MW appeared. Thus, reaction of the PN-1 variant produced distinct cysteine-PEGylated proteins containing increasing numbers of PEG units per protein molecule, up to 2 PEG per PN-1 molecule, the maximum number of cysteines available in the N99C;N140C PN-1 variant.

Distinct bands representing proteins increasing in relative molecular weight by 5,000 MW intervals is evidence of the specificity of the Maleimido-PEG reaction for attachment of PEG to cysteine residues. If the reaction had resulted in PEGylation of residues other than cysteine, a smear of proteins would appear on the

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gel, indicating the presence of proteins containing an infinite number of PEG moieties.

A sample of the cysteine-PEGylated protein which was reacted at a ratio of 2:1 Maleimido-PEG to protein was tested for activity using the assay described in D.4. This sample, which primarily contains cysteine-PEGylated protein, retained at least 100% of the activity of unmodified PN-1. The specific activity of the PEGylated proteins increased with an increasing amount of the Maleimido-PEG reagent present in the reaction mixture (Figure 4). These data suggest that an increase in activity is often found upon increasing PEG modification, which may result from the increased solubility and/or activity of PEGylated PN-1.

15 G.4 Generation of PEGylated PN-1 Mutant Using Conventional Method (Comparative Example)

In order to compare the results obtained above with the PEGylation methods known in the art, the N99C;N140C PN-1 variant was PEGylated using a method similar to that described by Zalipsky in USPN 5,122,614, with the substitution of a paranitrophenol carbonate of PEG for the N-succinimide carbonate of PEG used by Zalipsky as the activated carbonate. The protocol used was otherwise identical. Ratios ranging from 1:1 to 100:1 of activated PEG to PN-1 mutant (N99C;N140C) were used in the reactions.

A sample of each of the reacted mixtures containing dilutions of the PEGylation reagent was analyzed by SDS-PAGE. Analysis of this gel revealed that the amount of protein migrating at the molecular weight of the unmodified PN-1 variant decreased with increasing concentrations of the PEGylation reagent of Zalipsky used in the reaction. However, in contrast to the distinct bands generated using the method of the invention, a

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smear of proteins of various, increasing molecular weights appeared as the unmodified protein disappeared. The PEGylated proteins produced by the conventional method contained various numbers of PEG moieties per protein molecule, suggesting that attachment of PEG was random and that any number of lysine residues to various positions were modified.

The sample which contained various levels of PEG modification were tested for activity in the assay described in D.4. The data show that as the amount of the Maleimido-PEG reagent present in Maleimido-PEG/protein reaction mixture increased, the specific activity of the protein decreased (Figure 4). This suggests that increasing levels of PEG modification using the conventional method result in a decrease in the activity of the protein.

G.5 Activity of Cysteine-PEGylated PN-1 and PN-1 Mutants

The specific PN-1 mutants and cysteine-PEGylated mutants generated are shown in Table G.5A. Each of the PN-1 site-directed mutant proteins, as well as wild type PN-1, were modified by cysteine-PEGylation using the protocol described in F.2. The activity of wild type PN-1, each of the PN-1 site-directed mutants, and the cysteine-PEGylated wild type and mutant proteins was determined using the assay described in D.4.

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TABLE G.5A

		BEFORE PEG MODIFICATION		AFTER PEG MODIFICATION		
		SPECIFIC ACTIVITY ¹	REL TO WT ²	ACTIVITY	REL TO ACTIVITY BEFORE PEG ³	REL TO WT ²
MUTANT						
	WT	0.50	1	0.017	0.03	
	N99C	0.20	0.40	0.50	2.5	1.0
5	N140C	0.050	0.10	0.10	2	0.20
	N99C; N140C	0.167	.33	0.33	2	0.75
	S1C ⁵	0.10	0.20	0.25	2.5	0.50
	R63C ⁵	0.050	0.10	0.125	2.5	0.25
10	N85C ⁵	0.033	0.066	0.040	1.2	0.080
	D147C ⁵	0.063	0.125	0.125	2	0.25
	D192C ⁵	0.045	0.091	0.91	2	0.18
	E230C ⁵	0.071	0.14	0.20	2.8	0.40
	H252C ⁵	0.10	0.20	0.25	2.5	0.50
15	H252C ⁵	0.10	0.20	0.25	2.5	0.50
	N304C ⁵	0.056	0.11	0.17	3	0.33
	C117S; C131S; C209S	0.050		0.50		
20	1 Sp.Act is NIH units of thrombin inhibited per μ g PN-1 (variant).					
	2 Activity relative to wild type is calculated by dividing the activity of wild type PN-1 by the activity of the mutant.					
25	3 Activity of cysteine-PEGylated protein relative to activity of this protein before PEGylation is calculated by dividing the activity of the mutant before PEGylation by the activity of the mutant after PEGylation.					
30	4 Activity of cysteine-PEGylated PN-1 is variable as modification of the naturally occurring Cys 209 inhibits activity.					

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5 These mutants are in the N99C;N140C mutant background (i.e. these are triple mutants).

The mutations described here for PN-1 can be introduced into any serpin with the expectation of substantially similar effects due to the homology between the members of the serpin protein family.

G.6 Test for Half-Life of Cysteine-PEGylated PN-1 and PN-1 Mutants

The circulating half-life of any protein can be measured by standard methods well known in the art. For example, radioactive PEG-modified protein is injected into a mouse, rat, or rabbit. At various times, blood is withdrawn and the amount of protein remaining in circulation is determined by scintillation counting. Alternatively, PEG-modified PN-1 is injected into a mouse, rat, or rabbit. At various times, blood is withdrawn and urokinase inhibitory activity is measured. In some cases, the amount of protein remaining in circulation can be measured with antibody reaction as in an ELIZA or sandwich ELIZA.

G.7 Administration of Cysteine-PEGylated PN-1

Cysteine-PEGylated PN-1 and/or the cysteine-PEGylated PN-1 mutants described above may be used in the treatment of a variety of disease states for which PN-1 is indicated as therapeutically useful. For example, the proteins may be incorporated into a bandage for dressing a wound as described in USPN 5,196,196, herein incorporated by reference with respect to the use (e.g. dosages and routes of administration) of PN-1 in wound dressings. Alternatively, cysteine-PEGylated PN-1 and/or cysteine-PEGylated PN-1 mutants may be incorporated as the active ingredient(s) in a pharmaceutical compositions

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for treatment of inflammation and arthritis, as described in USPN 5,206,017 and USPN 5,326,562, each incorporated herein by reference with respect to the use (e.g. dosages and routes of administration) of PN-1 in treatment of
 5 such conditions.

EXAMPLE H

Generation of Cysteine-PEGylated Erythropoietin (EPO)

H.1 Selection of Amino Acid Residues for Cysteine Substitution

10 The amino acid sequence of erythropoietin (EPO) is as follows:

MGVHECPAWLWLLLSLLSLPLGLPVLGAPPRLICDSRVLQRYLLEAKEAE 50
 NITTGCAEHCSLNENITVPDTKVNIFYAWKRMEVGQQAVEVWQGLALLSEA 100
 VLRGQALLVNSSQPWEPLQLHVDKAVSGLRSLTTLRLALGAQKEAISPDP 150
 15 AASAAPLRTITADTFRKLFRVYSNFLRGKCLKLYTGEACRTGDR 194

The first 27 amino acids of the protein (italicized) are the EPO signal sequence. The amino acid residues which are in bold and underlined above (N24, N38, and N83) are sites of N-glycosylation in the native EPO protein.

20 These sites are thus selected for replacement with a cysteine residue, which is subsequently modified by PEGylation.

H.2 Site-directed Mutagenesis of EPO

25 The complete nucleotide sequence which codes for the mature EPO protein is known in the art and available from GenBank. DNA encoding the mature EPO protein is cloned and subjected to site-directed mutagenesis as described in D.2. Oligonucleotides for replacement of residues N24, N38, and N83 with cysteine are as follows:

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N24C: GCC AAG GAG GCC GAG **TGT** ATC ACG ACG GGC
N38C: TGC AGC TTG AAT GAG **TGT** ATC ACT GTC CCA
N83C: GCC CTG TTG GTC **TGC** TCT TCC CAG CCG

5 The residues in bold and underlined indicate the nucleotides which are different relative to the wild type EPO DNA sequence and represent the cysteine codon to be introduced into the EPO amino acid sequence.

10 The mutant EPO proteins which contain a cysteine residue at N24, N38, N83, or a combination of these site (e.g. double and triple mutants) are generated as described, expressed, and purified using techniques well known in the art.

H.3 Generation of Cysteine-PEGylated EPO and Cysteine-PEGylated EPO Mutants

15 Purified EPO mutants N24C, N38C, N83C, and mutants containing combinations of these mutations are subjected to cysteine-PEGylation using the protocol described in F.2. Samples of the reacted proteins are analyzed by SDS-PAGE to determine the extent of the PEGylation, as
20 well as the minimum amount of the Maleimido-PEG reagent necessary to produce fully PEGylated protein.

The activity of the cysteine-PEGylated wild type EPO, as well as the cysteine-PEGylated EPO mutants are tested using protocols known in the art.

EXAMPLE I

Generation of Cysteine-PEGylated Human Growth Hormone (hGH)

I.1 Selection of Amino Acid Residues for Cysteine Substitution

30 The nucleotide sequence, amino acid sequence, and the three-dimensional structure of human growth hormone

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(hGH) are well known in the art (see, for example, Cunningham and Wells 1989 *Science* 244:1081-1085). In addition, the three-dimensional structure of hGH bound to its receptor is known (De Vos et al. 1992 *Science* 5 255:306-312). Amino acid residues for replacement with cysteine are selected based upon the solvent-accessibility of the amino acid residue, the proximity of the residue to other amino acid residues with which it may interact, and the distance of the residue from 10 regions of hGH which are known to be important for receptor binding (Cunningham and Wells 1989 *Science* 244:1081-1085).

I.2 Site-directed Mutagenesis of hGH

Oligonucleotides for site-directed mutagenesis are 15 designed so as to introduce a cysteine residue in place of the amino acid residue(s) selected above. Site-directed mutagenesis is performed as described in D.2. The resulting hGH DNA is then inserted into an expression vector, and the resultant protein is expressed in *E. coli* 20 or other suitable host. The resulting hGH mutant protein is then purified according to methods known in the art.

I.3 Generation of Cysteine-PEGylated hGH

The hGH mutant protein is then subjected to cysteine-PEGylation using the method outlined in F.2. A 25 sample of a reacted mixture of Maleimido-PEG and hGH mutant protein is analyzed by SDS-PAGE to determine the optimal conditions for cysteine-PEGylation (e.g. the minimal amount of the Maleimido-PEG reagent necessary to provide the desired PEGylated hGH mutant protein).

30 The cysteine-PEGylated hGH protein is then tested for activity by assaying for the ability of the modified protein to bind to purified, truncated hGH receptor, as described in Cunningham and Wells (*ibid.*).

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EXAMPLE JGeneration of Hemoglobin by Cysteine-PEGylation
Cross-Linking

Hemoglobin is a tetrameric protein complex
5 composed of two "a" chains and two "b" chains. The amino
acid sequences of the "a" and "b" chains of hemoglobin,
as well as the tetrameric complex of hemoglobin composed
of 2 "a" and 2 "b" chains are well known. Appropriate
amino acid residues which are solvent-accessible and
10 minimally contacted with other side chains are selected
for site-directed mutagenesis to cysteine. The "a" and
"b" chain mutants are then expressed, purified, and
allowed to form a tetramer. The mutant tetrameric
complex is then reacted with various levels of
15 (Maleimido)₂-PEG as described in F.4 above. This reaction
can be carried out with very dilute hemoglobin levels to
form intramolecular cross-links to stabilize the
tetrameric form of hemoglobin, with a minimum number of
intermolecular cross-links. Alternatively, the reaction
20 can be carried out a higher with a higher hemoglobin
concentration, resulting in higher levels of
intermolecular cross-linking to stabilize an aggregate of
hemoglobin molecules.

While the present invention has been described
25 with reference to specific protease nexin-1 variants and
formulations containing such, it should be understood by
those skilled in the art that various changes may be made
and equivalence may be substituted without departing from
the true spirit and scope of the invention. In addition,
30 many modifications may be made to adapt a particular
situation, material, excipient, PN-1 variant, process,
process step or steps to the objective, spirit and scope
of the invention. All such modifications are intended to
be within the scope of the claims appended hereto.
35 WHAT IS CLAIMED IS:

CLAIMS:

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1 1. A protease nexin-1 variant wherein an amino
2 acid residue at a position selected from the group
3 consisting of P₄, P₃, P₂, P₁, P₁', P₂', P₃', P₄' is
4 replaced with a natural amino acid residue which is
5 different from the amino acid residue naturally present
6 at that position.

1 2. The protease nexin-1 variant of claim 1,
2 wherein the variant has a different protease specificity
3 as compared with protease nexin-1 and/or an increased
4 rate association constant with respect to a specific
5 protease as compared with protease nexin-1.

1 3. A protease nexin-1 variant wherein amino acid
2 residues at the active site of protease nexin-1 are
3 replaced with an equivalent number of active site amino
4 acid residues of a serine protease inhibitor other than
5 protease nexin-1.

1 4. The variant of claim 3, wherein the serine
2 protease inhibitor is selected from the group consisting
3 of antithrombin III, heparin cofactor II, α -1-
4 antitrypsin, α -1-protease inhibitor, plasminogen
5 activator inhibitor I, II, & III, α -2-antiplasmin,
6 kallikrein-binding protein, and C1-inhibitor.

1 5. The variant of claim 3, wherein amino acid
2 residues at positions P₄, P₃, P₂, P₁, P₁', P₂', P₃', P₄'
3 of the active site of protease nexin-1 are replaced with
4 an amino acid sequence selected from the group consisting
5 of:

	P ₄	P ₃	P ₂	P ₁	P ₁ '	P ₂ '	P ₃ '	P ₄ '
7	Val-	Ser-	Ala-	Arg	Met-	Ala-	Pro-	Glu
8	Met-	Thr-	Gly-	Arg	Thr-	Gly-	His-	Gly
9	Phe-	Thr-	Phe-	Arg	Ser-	Ala-	Arg-	Leu
10	Ile-	Ala-	Gly-	Arg	Ser-	Leu-	Asn-	Pro

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11	Ala- Met- Ser- Arg	Met- Ser- Leu- Ser
12	Ser- Val- Ala- Arg	Thr- Leu- Leu- Val
13	Ile- Leu- Ser- Arg	Arg- Thr- Ser- Leu
14	Phe- Arg- Ile- Leu	Ser- Arg- Arg- Thr
15	Ala- Ile- Pro- Met	Ser- Ile- Pro- Pro
16	Glu- Lys- Ala- Trp	Ser- Lys- Tyr- Gln
17	Leu- Leu- Ser- Ala	Leu- Val- Glu- Thr
18	Ile- Thr- Leu- Leu	Ser- Ala- Leu- Val
19	Phe- Met- Pro- Leu	Ser- Thr- Glu- Val
20	Met- Thr- Gly- Arg	Thr- Gly- His- Gly.

1 6. A protease nexin-1 variant wherein three or
2 more amino acid residues of the active site of protease
3 nexin-1 are replaced with different amino acid residues
4 which comprise a substrate sequence specific for a given
5 protease.

1 7. The variant of claim 6, wherein the given
2 protease is selected from the group consisting of
3 elastase, cathepsin G, C1-esterase, thrombin, kallikrein,
4 and Factor Xa, Factor IXa, Factor XIa, Factor XIIa,
5 Factor VIIIa, Factor V', Activated Protein C, trypsin,
6 chymotrypsin.

1 8. A protein or portion thereof containing three
2 or more amino acids, at least one of which is cysteine,
3 wherein polyethylene glycol is covalently bound to a thio
4 group of the cysteine.

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1 9. A modified protein comprised of the amino
2 acid sequence of a naturally occurring protein which
3 sequence includes at least one cysteine residue wherein
4 the modification comprises the coupling of polyethylene
5 glycol to a cysteine residue of the protein.

1 10. A method of coupling polyethylene glycol to a
2 protein comprising the steps of:
3 identifying a protein of interest and
4 determining a site for coupling of polyethylene glycol to
5 the protein;
6 coupling polyethylene glycol to the protein
7 at said site wherein the polyethylene glycol is
8 covalently bound to a thio group of a cysteine residue of
9 the protein.

1 11. The method of claim 10, wherein the cysteine
2 residue is naturally present in the protein.

1 12. The method of claim 10, wherein the protein
2 is altered to include a cysteine residue not normally
3 present and the polyethylene glycol is covalently bound
4 to the added cysteine residue.

1 13. The method of claim 12 wherein the site for
2 coupling of polyethylene glycol is within a solvent
3 accessible region of the protein.

1 14. The method of claim 12 wherein the protein is
2 altered to include the cysteine residue at a site of
3 glycosylation.

1 15. The method of claim 12, wherein the protein
2 is altered to include multiple cysteine residues.

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1 16. The method of claim 10 wherein said
2 polyethylene glycol comprises at least two
3 protein-reactive moieties.

1 17. The method of claim 10, wherein said
2 polyethylene glycol is between 200 and 10,000 molecular
3 weight.

1 18. The method of claim 10, wherein the protein
2 of interest is protease nexin-1.

1 19. The method of claim 10, wherein the protein
2 of interest is a protease nexin-1 variant, said variant
3 having an amino acid residue at a position selected from
4 the group consisting of P₄, P₃, P₂, P₁, P₁', P₂', P₃' and
5 P₄' replaced with a natural amino acid residue which is
6 different from the amino acid residue naturally present
7 at that position.

1 20. The method of claim 10, wherein the protein
2 of interest is a protease nexin-1 variant wherein at
3 least one amino acid residue at the active site of
4 protease nexin-1 is replaced with an equivalent number of
5 active site amino acid residues of a serine protease
6 inhibitor other than protease nexin-1.

1 21. The method of claim 10, wherein the protein
2 of interest is a protease nexin-1 variant wherein three
3 or more amino acid residues of the active site of
4 protease nexin-1 are replaced with different amino acid
5 residues which comprise a substrate sequence specific for
6 a given protease.

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1 22. A modified protease nexin-1 protein comprised
2 of the amino acid sequence of naturally occurring
3 protease nexin-1 protein which sequence includes at least
4 one cysteine residue, wherein the modification comprises
5 the coupling of polyethylene glycol to a cysteine residue
6 of the protein.

1 23. A modified protease nexin-1 variant comprised
2 of the amino acid sequence of protease nexin-1, wherein
3 an amino acid residue at a position selected from the
4 group consisting of P_4 , P_3 , P_2 , P_1 , P_1' , P_2' , P_3' and P_4' is
5 replaced with a natural amino acid residue which is
6 different from the amino acid residue naturally present
7 at that position, and which sequence includes at least
8 one cysteine residue, wherein the modification comprises
9 the coupling of polyethylene glycol to a cysteine residue
10 of the protein.

1 24. The modified protease nexin-1 variant protein
2 of claim 23, wherein the variant has a different protease
3 specificity as compared with protease nexin-1 and/or an
4 increased rate association constant with respect to a
5 specific protease as compared with protease nexin-1.

1 25. A modified protease nexin-1 variant wherein
2 amino acid residues at the active site of protease nexin-
3 1 are replaced with an equivalent number of active site
4 amino acid residues of a serine protease inhibitor other
5 than protease nexin-1, and the amino acid sequence of the
6 variant protein includes at least one cysteine residue,
7 wherein the modification comprises the coupling of
8 polyethylene glycol to a cysteine residue of the protein.

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1 26. The modified variant of claim 25, wherein the
2 serine protease inhibitor is selected from the group
3 consisting of antithrombin III, heparin cofactor II, α -1-
4 protease inhibitor, plasminogen activator inhibitor I,
5 II, & III, α -2-antiplasmin, kallikrein-binding protein,
6 and C1-inhibitor.

1 27. The modified variant of claim 25, wherein
2 amino acid residues at positions P_4 , P_3 , P_2 , P_1 , P_1' , P_2' ,
3 P_3' and P_4' of the active site of protease nexin-1 are
4 replaced with an amino acid sequence selected from the
5 group consisting of:

	P_4	P_3	P_2	P_1	P_1'	P_2'	P_3'	P_4'
6	Val-	Ser-	Ala-	Arg	Met-	Ala-	Pro-	Glu
7	Met-	Thr-	Gly-	Arg	Thr-	Gly-	His-	Gly
8	Phe-	Thr-	Phe-	Arg	Ser-	Ala-	Arg-	Leu
9	Ile-	Ala-	Gly-	Arg	Ser-	Leu-	Asn-	Pro
10	Ala-	Met-	Ser-	Arg	Met-	Ser-	Leu-	Ser
11	Ser-	Val-	Ala-	Arg	Thr-	Leu-	Leu-	Val
12	Ile-	Leu-	Ser-	Arg	Arg-	Thr-	Ser-	Leu
13	Phe-	Arg-	Ile-	Leu	Ser-	Arg-	Arg-	Thr
14	Ala-	Ile-	Pro-	Met	Ser-	Ile-	Pro-	Pro
15	Glu-	Lys-	Ala-	Trp	Ser-	Lys-	Tyr-	Gln
16	Leu-	Leu-	Ser-	Ala	Leu-	Val-	Glu-	Thr
17	Ile-	Thr-	Leu-	Leu	Ser-	Ala-	Leu-	Val
18	Phe-	Met-	Pro-	Leu	Ser-	Thr-	Glu-	Val
19	Met-	Thr-	Gly-	Arg	Thr-	Gly-	His-	Gly
20								

21 and the variant protein contains at least one cysteine
22 residue, wherein the modification comprises the coupling
23 of polyethylene glycol to a cysteine residue of the
24 protein.

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1 28. A modified protease nexin-1 variant wherein
2 three or more amino acid residues of the active site of
3 protease nexin-1 are replaced with different amino acid
4 residues which comprise a substrate sequence specific for
5 a given protease and the amino acid sequence of the
6 variant protein includes at least one cysteine residue
7 wherein the modification comprises the coupling of
8 polyethylene glycol to a cysteine residue of the protein.

1 29. The modified protease nexin-1 variant of
2 claim 28, wherein the given protease is selected from the
3 group consisting of elastase, cathepsin G, C1-esterase,
4 thrombin, kallikrein, Factor Xa, Factor IXa, Factor
5 XXIIa, Factor VIIIIa, Factor V', Activated Protein C,
6 trypsin, and chymotrypsin.

1 30. A compound having the following general
2 structural formula:
3
$$R_1-S-PEG-S-R_2$$

4 wherein R_1 and R_2 are independently each an amino acid
5 sequence, each S is a thio group of a cysteine residue of
6 each of R_1 and R_2 , and PEG is polyethylene glycol.

1 31. The compound of claim 30, wherein R_1 and R_2
2 each independently comprise from about 6 to 1,000 amino
3 acids.

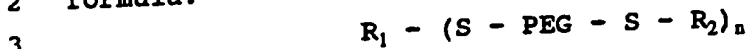
1 32. The compound of claim 30, wherein said
2 polyethylene glycol is from 200 to 10,000 molecular
3 weight.

1 33. The compound of claim 30, wherein in R_1 and
2 R_2 are the same.

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1 34. The compound of claim 30, wherein R₁ is
2 hemoglobin a chain and R₂ is hemoglobin b chain.

1 35. A compound having the following general
2 formula:



4 wherein R₁ and R₂ are independently each amino acid
5 sequences, S is a thio group of a cysteine residue of
6 each of R₁ and R₂, and PEG is polyethylene glycol.

1 36. The compound of claim 35, wherein said
2 polyethylene glycol is from 200 to 10,000 molecular
3 weight.

1 37. The compound of claim 35, wherein R₁ and R₂
2 are the same.

1 38. The compound of claim 37, wherein R₁ is
2 hemoglobin a chain and R₂ is hemoglobin b chain.

1 39. A DNA sequence encoding the protease nexin-1
2 variant of claim 1.

 40. A DNA sequence encoding the protease nexin-1
variant of claim 2.

1 41. A DNA sequence encoding the protease nexin-1
2 variant of claim 4.

1 42. A DNA sequence encoding the protease nexin-1
2 variant of claim 5.

1 43. A DNA sequence encoding the chimeric protease
2 of claim 8.

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1 44. A pharmaceutical composition, comprising:
2 a pharmaceutically acceptable carrier; and
3 a variant of protease nexin-1 as claimed in
4 claim 1.

1 45. A pharmaceutical composition, comprising:
2 a pharmaceutically acceptable carrier; and
3 a variant of protease nexin-1 as claimed in
4 claim 2.

1 46. A pharmaceutical composition, comprising:
2 a pharmaceutically acceptable carrier; and
3 a variant of protease nexin-1 as claimed in
4 claim 4.

1 47. A pharmaceutical composition, comprising:
2 a pharmaceutically acceptable carrier; and
3 a variant of protease nexin-1 as claimed in
4 claim 5.

1 48. A method of producing a variant protein,
2 comprising:
3 connecting DNA encoding amino acids of a
4 receptor binding region of a first naturally occurring
5 protein with DNA encoding amino acids of a second protein
6 or a biologically active portion thereof which is
7 different from the first protein; and
8 expressing the DNA in a suitable host.

1 49. The variant of claim 48, wherein the second
2 protein is a variant of PN-1 wherein an amino acid
3 residue at a position selected from the group consisting
4 of P4, P3, P2, P1, P1', P2', P3', P4' is replaced with a
5 natural amino acid residue which is different from the
6 amino acid residue naturally present at that position.

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50. A method as in claim 48 wherein the receptor binding region is from a first protein selected from the group consisting of urokinase, tPA, Factor IX, Factor X, Protein C, Epidermal growth factor and EGF-like domains.

1 51. A method as in claim 50 wherein the receptor-
2 binding region is an amino terminal fragment of
3 urokinase.

1 52. A method as in claim 51 where the receptor-
2 binding region is an amino terminal fragment of urokinase
3 including amino acids 1-135 or 1-87.

1 53. A pharmaceutical composition, comprising:
2 a pharmaceutically acceptable carrier; and
3 a protein or portion thereof as claimed in
4 claim 8.

SEQUENCE OF PROTEASE NEXIN I TYPE ALPHA

CTGTGACCCCTCCTCGCGCCGCGCTTCGCTCGCTCCGACTCCCGCGCGCGAGACTAGGCTCCGCTCCGGTTGCGGCGGACCCCTCCGCGGCGCCCTG66GATCCAGCGAGCGG

CGGTGCGTCCCTTGTTGGTGAAGGAACC
 S10
 ATG AAC TGG CAT CTC CCC CTC TTC CTC TTT GGC TCT GTG ACG CTG CCT TCC ATC TGC TCC CAC TTC AAT
 Met Asn Trp His Leu Pro Leu Phe Leu Leu Ala Ser Val Thr Leu Pro Ser Ile Cys Ser His Phe Asn

CCT CTG TCT CTC GAG GAA CTA GGC TCC AAC ACG GGG ATC CAG GTT TTC AAT CAG ATT GTG AAG TCG AGG CCT CAT GAC AAC ATC GTG ATC
 Pro Leu Ser Leu Glu Glu Leu Gly Ser Asn Thr Gly Ile Gln Val Phe Asn Gln Ile Val Lys Ser Arg Pro His Asp Asn Ile Val Ile

TCT CCC CAT GGG ATT GCG TCG GTC CTG GGG ATG CTT CAG CTG GGG GCG GAC GGC AGG ACC AAG AAG CAG CTC GCC ATG GTG ATG AGA TAC
 Ser Pro His Gly Ile Ala Ser Val Leu Gly Met Leu Gln Leu Gly Ala Asp Gly Arg Thr Lys Lys Gln Leu Ala Met Val Met Arg Tyr

GGC GTA AAT GGA GTT GGT AAA ATA TTA AAG AAG ATC AAC AAG GCC ATC GTC TCC AAG AAG AAT AAA GAC ATT GTG ACA GTG GCT AAC GCC
 Gly Val Asn Gly Val Gly Lys Ile Leu Lys Lys Ile Asn Lys Ala Ile Val Ser Lys Lys Asn Lys Asp Ile Val Thr Val Ala Asn Ala

GTG TTT GTT AAG AAT GCC TCT GAA ATT GAA GTG CCT TTT GTT ACA AGG AAC AAA GAT GTG TTC CAG TGT GAG GTC CGG AAT GTG AAC TTT
 Val Phe Val Lys Asn Ala Ser Glu Ile Glu Val Pro Phe Val Thr Arg Asn Lys Asp Val Phe Gln Cys Glu Val Arg Asn Val Asn Phe

GAG GAT CCA GCC TCT GCG TGT GAT TCC ATC AAT GCA TGG GTT AAA AAT GAA ACC AGG GAT ATG ATT GAC AAT CTG CTG TCC CCA GAT CTT
 Glu Asp Pro Ala Ser Ala Cys Asp Ser Ile Asn Ala Trp Val Lys Asn Glu Thr Arg Asp Met Ile Asp Asn Leu Ser Pro Asp Leu

ATT GAT GGT GTG CTC ACC AGA CTG GTC CTC GTC AAC GCA GTG TAT TTC AAG GGT CTG TGG AAA TCA CGG TTC CAA CCC GAG AAC ACA AAG
 Ile Asp Gly Val Leu Thr Arg Leu Val Leu Val Asn Ala Trp Val Tyr Phe Lys Gly Leu Trp Lys Ser Arg Phe Gln Pro Glu Asn Thr Lys

AAA CGC ACT TTC GTG GCA GCC GAC GGG AAA TCC TAT CAA GTG CCA ATG CTG GCC CAG CTC TCC GTG TTC CGG TGT GGG TCG ACA AGT GCC
 Lys Arg Thr Phe Val Ala Ala Asp Gly Lys Ser Tyr Gln Val Pro Met Leu Ala Gln Leu Ser Val Phe Arg Cys Gly Ser Thr Ser Ala

CCC AAT GAT TTA TGG TAC AAC TTC ATT GAA CTG CCC TAC CAC GGG GAA AGC ATC AGC ATG CTG ATT GCA CTG CCG ACT GAG AGC TCC ACT
 Pro Asn Asp Leu Trp Tyr Asn Phe Ile Glu Leu Pro Tyr His Gly Glu Ser Ile Ser Met Leu Ile Ala Leu Pro Thr Glu Ser Ser Thr

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FIG. 1-1

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250 CCG CTG TCT GCC ATC ATC CCA CAC ATC AGC ACC AAG ACC ATA GAC AGC IGG ATG AGC ATC ATG GTG CCC AAG AGG GTG CAG GTG ATC CTC
Pro Leu Ser Ala Ile Ile Pro His Ile Ser Thr Lys Thr Lys Thr Lys Thr Lys Thr Lys Thr Lys Arg Val Gln Val Ile Leu

280 CCC AAG TTC ACA GCT GTA GCA CAA ACA GAT TTG AAG GAG CCG CTG AAA GTT CTT GGC ATT ACT GAC ATG TTT GAT TCA TCA AAG GCA AAT
Pro Lys Phe Thr Ala Val Ala Val Ala Gln Thr Asp Leu Lys Glu Pro Leu Lys Lys Val Leu Gly Ile Thr Asp Met Phe Asp Ser Ser Lys Ala Asn

310 TTT GCA AAA ATA ACA AGG TCA GAA AAC CTC CAT GTT TCT CAT ATC TIG CAA AAA GCA AAA ATT GAA GTC AGT GAA GAT GGA ACC AAA GCT HindIII
Phe Ala Lys Ile Thr Arg Ser Glu Asn Leu Leu His Val Ser His Ile Leu Gln Lys Ala Lys Ile Glu Val Ser Glu Asp Gly Thr Lys Ala

340 TCA GCA GCA ACA ACT GCA ATT CTC ATT GCA AGA TCA TCG CCT CCC TGG TTT ATA GTA GAC AGA CCT TTT CTG TTT TTC ATC CGA CAT AAT
Ser Ala Ala Thr Thr Ala Ile Leu Ile Ala Arg Ser Ser Pro Pro Trp Phe Ile Val Asp Arg Pro Phe Leu Phe Ile Arg His Asn

370 CCT ACA-GGT GCT GTG TTA TTC ATG GGG CAG ATA AAC AAA CCC TGA AGAGTATACAAGAACCATGCAAGCAACGACTACTTTGCTACGAAGAAGACTCCT
Pro Thr Gly Ala Val Leu Phe Met Gly Gln Ile Asn Lys Pro ---

378
TTCCGTCATCTTTCGTTAAATATCTTGATCATCGCATCTTTTCAAACGCTAGTTTCTTAGGAAGCAGACTCGATGCAACTGTTCTGTTCTGGAGGTATTGGAGGGAAAAACA
AGCAGGATGCGCTGGCACAGCTGCTAGGATTGATATAGAAGACTTCCAGATGCCCTAAAAGATTCITTAARACTACTGAAGTGTACCTAGGTTAACATCCCTGTTGAGGTATTGCT
GTTTGTCAGTTAGGAATTTTGTGTTTGTCTCTATGTCGGCTTTTICAGAAGAAATTAATCAGTGTGACAGAAAAAAAATGTTTTATGAGTCTTTTACTTTTTATGAAA
AAAAAATATTTGTTCCTTTTAAATCTTTTCCCCCATCCCTCCAAAGCTTGATAGCAAGCGTTATTTTGGGGGTAGAAACGGTGAAATCTCTAGCCTCTTTGTGTTTTGTGTT
GTTGTTGTTGTTTTTATAATGCAATGATTCACIAAAATAAAATTTAAAAAACGTCCTGCTGCTAGACAAGGTTGTGCATGTGCGCTGCTCACTACTGAGTCTGCTACCTATGGA
TTTGCATTTTTGTATTTGTACAAAGTAAAAATAACT

SUBSTITUTE SHEET (RULE 26)

FIG. 1-2

SEQUENCE OF PROTEASE NEXIN 1 TYPE BETA

CTGTGACCCCTCCTCGCGCGCGCTTCCTCGCTCCTCGACTCCCGCGCGCGAGACTAGGCTCCGCTCGGTTGCGGCGACCCCTCCGCGCGCCCTCGGGATCCAGCGAGCG

CGGTCGTCCTTGGTGGAGGAACC ^{S1} ATG AAC TGG CAT CTC CCC CTC TTC CTC TTG GCC TCT GTG ACG CTG CCT ICC ATC TGC TCC CAC TTC AAT ¹
Met Asn Trp His Leu Pro Leu Phe Leu Leu Ala Ser Val Thr Leu Pro Ser Ile Cys Ser His Phe Asn

CCT CTG TCT CTC GAG GAA CTA GGC TCC AAC ACG GGG ATC CAG GTT TTC AAT CAG ATT GTG AAG TCG AGG CCT CAT GAC AAC ATC GTG ATC ³⁰
Pro Leu Ser Leu Glu Glu Leu Gly Ser Asn Thr Gly Ile Gln Val Phe Asn Gln Ile Val Lys Ser Arg Pro His Asp Asn Ile Val Ile

TCT CCC CAT GGG ATT GCG TCG GTC CTG GGG ATG CTT CAG CTG GGG GCG GAC GGC AGG ACC AAG AAG CAG CTC GCC ATG GTG ATG AGA TAC ⁶⁰
Ser Pro His Gly Ile Ala Ser Val Leu Gly Met Leu Gln Leu Gly Ala Asp Gly Arg Thr Lys Lys Gln Leu Ala Met Val Met Arg Tyr

GGC GTA AAT GGA GTT GGT AAA ATA TTA AAG AAG ATC AAC AAG GCC ATC GTC TCC AAG AAG AAT AAA GAC ATT GTG ACA GTG GCT AAC GCC ⁹⁰
Gly Val Asn Gly Val Gly Lys Ile Leu Lys Lys Ile Asn Lys Ala Ile Val Ser Lys Lys Asn Lys Asp Ile Val Thr Val Ala Asn Ala

GTG TTT GTT AAG AAT GAA ATT GAA GTG CCT TTT GTT ACA AGG AAC AAA GAT GTG TTC CAG TGT GAG GTC CGG AAT GTG AAC TTT ¹²⁰
Val Phe Val Lys Asn Ala Ser Glu Ile Glu Val Thr Arg Asn Lys Asn Lys Asp Val Phe Gln Cys Glu Val Arg Asn Val Asn Phe

GAG GAT CCA GCC TCT GCC TGT GAT TCC ATC AAT GCA TGG GTT AAA AAT GAA ACC AGG GAT ATG ATT GAC AAT CTG CTG TCC CCA GAT CTT ¹⁵⁰
Glu Asp Pro Ala Ser Ala Cys Asp Ser Ile Asn Ala Trp Val Lys Asn Glu Thr Arg Asp Met Ile Asp Asn Leu Leu Ser Pro Asp Leu

ATT GAT GGT GTG CTC ACC AGA CTG GTC CTC GTC AAC GCA GTG TAT TTC AAG GGT CTG TGG AAA TCA CGG TTC CAA CCC GAG AAC ACA AAG ¹⁸⁰
Ile Asp Gly Val Leu Thr Arg Leu Val Leu Val Asn Ala Trp Val Tyr Phe Lys Gly Leu Trp Lys Ser Arg Phe Gln Pro Glu Asn Thr Lys

AAA CGC ACT TTC GTG GCA GCC GAC GGG AAA TCC TAT CAA GTG CCA ATG CTG GCC CAG CTC TCC GTG TTC CGG TGT GGG TCG ACA AGT GCC ²¹⁰
Lys Arg Thr Phe Val Ala Ala Asp Gly Lys Ser Tyr Gln Val Pro Met Leu Ala Gln Leu Ser Val Phe Arg Cys Gly Ser Thr Ser Ala

CCC AAT GAT TTA TGG TAC AAC TTC ATT GAA CTG CCC TAC CAC GGG GAA AGC ATC AGC ATG CTG ATT GCA CTG CCG ACT GAG AGC TCC ACT ²⁴⁰
Pro Asn Asp Leu Trp Tyr Asn Phe Ile Glu Leu Pro Tyr His Gly Glu Ser Ile Ser Met Leu Ile Ala Leu Pro Thr Glu Ser Ser

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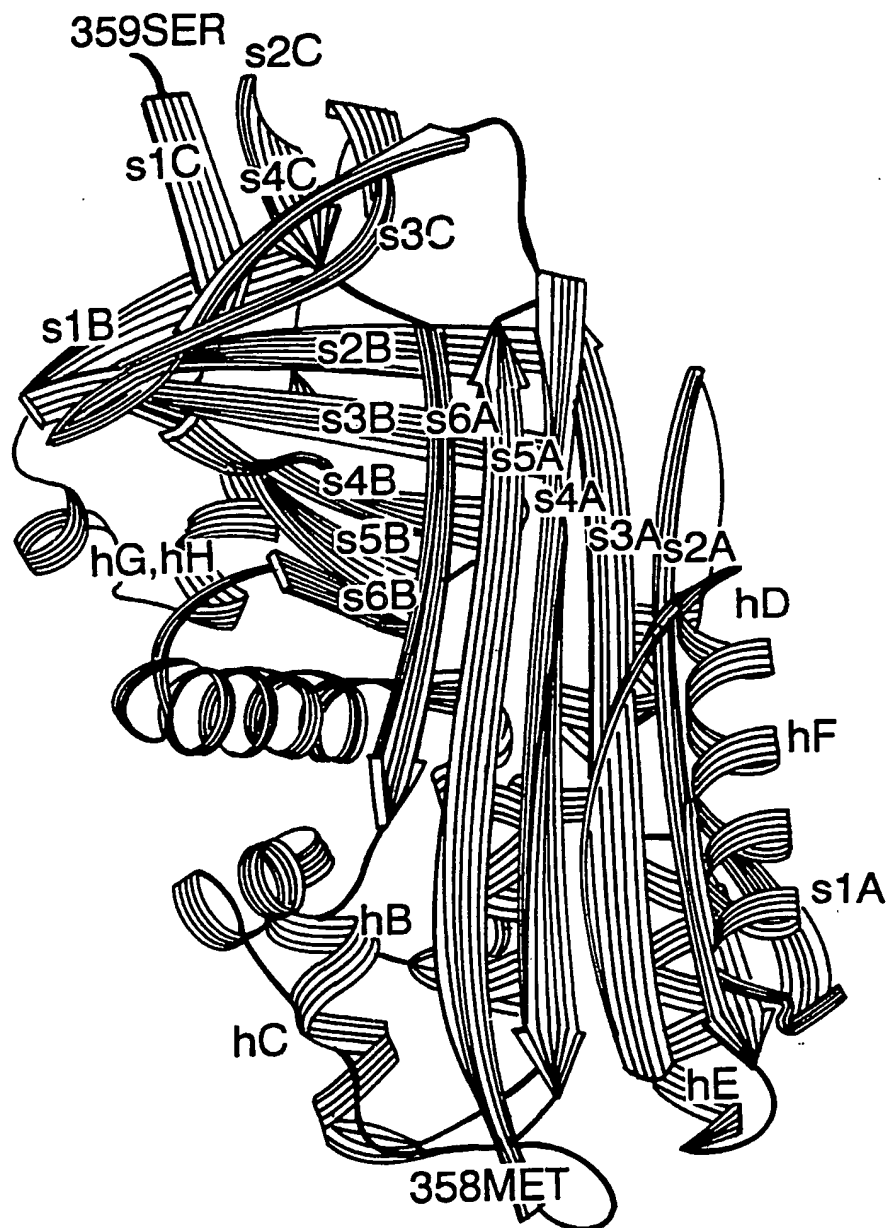
FIG. 2-1

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250 CCG CTG TCT GCC ATC ATC CCA CAC ATC AGC ACC AAG ACC ATA GAC AGC TGG ATG AGC ATC ATG GTG CCC AAG AGG GTG CAG GTG ATC CTG
 Pro Leu Ser Ala Ile Ile Pro His Ile Ser Thr Lys Thr Ile Asp Ser Trp Met Ser Ile Met Val Pro Lys Arg Val Gln Val Ile Leu
 260
 280 CCC AAG TTC ACA GCT GTA GCA CAA ACA GAT TTG AAG GAG CCG CTG AAA GTT CTT GGC ATT ACT GAC ATG TTT GAT TCA TCA AAG GCA AAT
 Pro Lys Phe Thr Ala Val Ala Gln Thr Asp Leu Lys Lys Glu Pro Leu Lys Val Leu Gly Ile Thr Asp Met Phe Asp Ser Ser Lys Ala Asn
 290
 310 TTT GCA AAA ATA ACA ACA GGG TCA GAA AAC CTC CAT GTT TCT CAT ATC TTG CAA AAA GCA AAA ATT GAA GTC AGT GAA GAT GGA ACC AAA
 Phe Ala Lys Ile Thr Thr Thr Gly Ser Glu Asn Leu His Val Ser His Ile Leu Gln Lys Ala Lys Ile Glu Val Ser Glu Asp Gly Thr Lys
 320 HindIII
 340 GCT TCA GCA GCA ACA ACT GCA ATT CTC ATT GCA AGA TCA TCG CCT CCC TGG TTT ATA GTA GAC AGA CCT TTT CTG TTT TTC ATC CGA CAT
 Ala Ser Ala Ala Thr Thr Ala Ile Leu Ile Ala Arg Ser Ser Pro Pro Trp Phe Ile Val Asp Arg Pro Phe Leu Phe Phe Ile Arg His
 350
 370 AAT CCT ACA GGT GCT GTG TTA TTC ATG GGG CAG ATA AAC AAA CCC TGA AGAGTATACAAAGAAACCATGCAAAAGCAACGACTACTTTTGCTACGAAGAAAGACT
 Asn Pro Thr Gly Ala Val Leu Phe Met Gly Gln Ile Asn Lys Pro ---
 378
 CATTCTGCATCTTCTGTTAAATATTCITGTACATCGCATTCCTTTTCAAAACGTAGTTTCTTAGGARGCAGACTCGATGCAACTGTTCCCTGTTCTGGAGGTATTGGAGGGAAAAA
 ACAAGCAGGATGCCTGGCAGCTGTACTGAGGATTGATATAGAAAGACTCCAGATGCCATAAAGATTCTTTAAACTACTGAACTGTTACCTAGGTTAACATCCCTGTTGAGGTATTT
 GCTGTTTGCCAGTTAGGAATTTTGTGTTGTTGCTCTATATGTGCGGCTTTTCAGAGAAATTTAATCAGTGTGACAGAAAAAAATGTTTTATGGTAGCTTTTACTTTTTATG
 AAAAAAAATTAATTTGTTCTTTTAAATCTTTTCCCCCATCCCTCCAAAGCTTTGATAGCAAGCGTTATTTTGGGGGTAGAAACGGTGAAATCTCTAGCCTCTTTGTTTTGTT
 GTTGTGTTGTTGTTTATATAATGCATGTATTCACATAAAATAAAATTTAAAAAACGTCCTGCTCTGTAGACAAGGTTGTGCATGTGCTGCTACTGAGTCTGCTACCTAT
 GGATTTGCATTTTGTATTGTACAAAGTAAAAATAACT

FIG. 2-2

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**FIG. 3**

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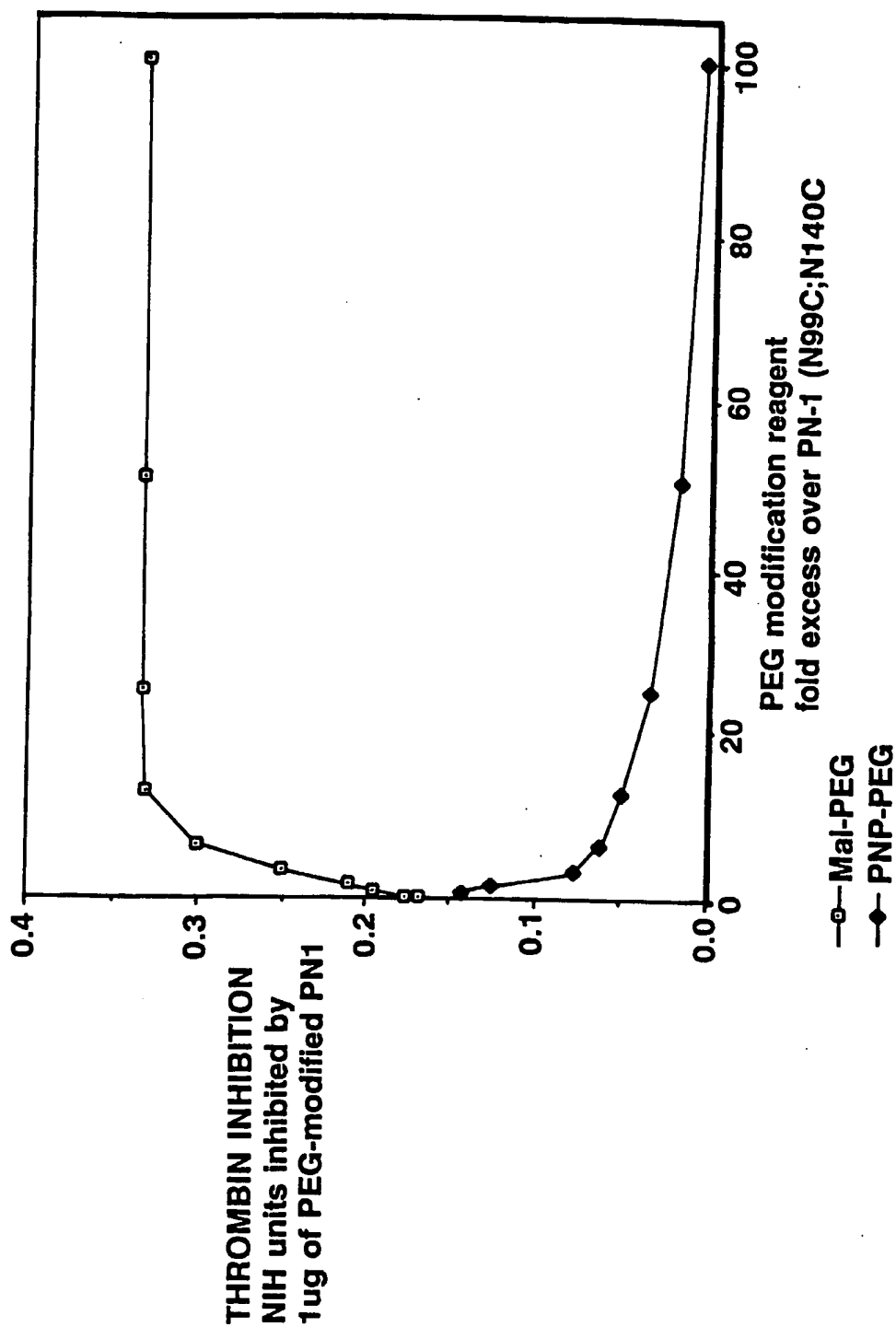


FIG. 4

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US94/11624**A. CLASSIFICATION OF SUBJECT MATTER**

IPC(6) : C12P 21/06; C12N 15/00, 9/96; A61K 38/00

US CL : 435/69.2, 69.7, 172.1, 188; 530/345

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

U.S. : 435/69.2, 69.7, 172.1, 188; 530/345

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	US, A, 5,166,322 (SHAW ET AL.) 24 November 1992, see entire document.	1-53
Y	US, A, 5,206,344 (KATRE ET AL.) 27 April 1993, see entire document.	1-53

☐ Further documents are listed in the continuation of Box C. ☐ See patent family annex.

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*O document referring to an oral disclosure, use, exhibition or other means	
*P document published prior to the international filing date but later than the priority date claimed	

Date of the actual completion of the international search

09 FEBRUARY 1995

Date of mailing of the international search report

17 FEB 1995

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